L Number	Hits	Search Text	DB	Time stamp
1	0	liu-qingyun.in	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/02/06 08:28
2	7	liu-qingyun.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/02/06 08:28
3	3	mcdonald-terrence-p.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/02/06 08:28
4	2	hg51	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/02/06 08:29

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspta1649jxm

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Apr 08	"Ask CAS" for self-help around the clock
NEWS 3	Jun 03	New e-mail delivery for search results now available
NEWS 4	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 5	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS 6	Aug 26	Sequence searching in REGISTRY enhanced
NEWS 7	Sep 03	JAPIO has been reloaded and enhanced
NEWS 8	Sep 16	Experimental properties added to the REGISTRY file
NEWS 9	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 10	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 11	Oct 24	BEILSTEIN adds new search fields
NEWS 12	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 13	Nov 18	DKILIT has been renamed APOLLIT
NEWS 14	Nov 25	More calculated properties added to REGISTRY
NEWS 15	Dec 04	CSA files on STN
NEWS 16	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 17	Dec 17	TOXCENTER enhanced with additional content
NEWS 18	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS 19	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS 20	Feb 13	CANCERLIT is no longer being updated
NEWS 21	Feb 24	METADEX enhancements
NEWS 22	Feb 24	PCTGEN now available on STN
NEWS 23	Feb 24	TEMA now available on STN
NEWS 24	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS 25	Feb 26	PCTFULL now contains images
NEWS 26	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
NEWS 27	Mar 20	EVENTLINE will be removed from STN
NEWS 28	Mar 24	PATDPAFULL now available on STN
NEWS 29	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS 30	Apr 11	Display formats in DGENE enhanced
NEWS 31	Apr 14	MEDLINE Reload
NEWS 32	Apr 17	Polymer searching in REGISTRY enhanced
NEWS 33	Apr 21	Indexing from 1947 to 1956 being added to records in CA/CAPLUS
NEWS 34	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
NEWS 35	Apr 28	RDISCLOSURE now available on STN
NEWS 36	May 05	Pharmacokinetic information and systematic chemical names added to PHAR
NEWS 37	May 15	MEDLINE file segment of TOXCENTER reloaded
NEWS 38	May 15	Supporter information for ENCOMPPAT and ENCOMPLIT updated
NEWS 39	May 16	CHEMREACT will be removed from STN
NEWS 40	May 19	Simultaneous left and right truncation added to WSCA
NEWS 41	May 19	RAPRA enhanced with new search field, simultaneous left and right truncation

NEWS EXPRESS April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 09:57:22 ON 28 MAY 2003

=> file medline biosis embase caplus
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 09:57:38 ON 28 MAY 2003

FILE 'BIOSIS' ENTERED AT 09:57:38 ON 28 MAY 2003
COPYRIGHT (C) 2003 BIOLOGICAL ABSTRACTS INC.(R)

FILE 'EMBASE' ENTERED AT 09:57:38 ON 28 MAY 2003
COPYRIGHT (C) 2003 Elsevier Science B.V. All rights reserved.

FILE 'CAPLUS' ENTERED AT 09:57:38 ON 28 MAY 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

=> s liu qingyun /au
L1 91 LIU QINGYUN

=> s mcdonald terrence /au
L2 7 MCDONALD TERRENCE

=> s l1 and l2
L3 2 L1 AND L2

=> d l3 total ibib

L3 ANSWER 1 OF 2 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:204159 BIOSIS
DOCUMENT NUMBER: PREV199900204159
TITLE: Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9.
AUTHOR(S): Ng, Gordon Y. K. (1); **McDonald, Terrence**; Bonnert, Tim; Rigby, Michael; Heavens, Robert; Whiting, Paul; Chateauneuf, Anne; Coulombe, Nathalie; Kargman, Stacia; Caskey, Thomas; Evans, Jilly; O'Neill, Gary P.; **Liu, Qingyun**
CORPORATE SOURCE: (1) Department of Biochemistry and Molecular Biology, Merck

Frosst Center for Therapeutic Research, 16711 TransCanada Highway, Kirkland, PQ, H9H 3L1 Canada
SOURCE: Genomics, (March 15, 1999) Vol. 56, No. 3, pp. 288-295. ISSN: 0888-7543.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L3 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:191160 CAPLUS
DOCUMENT NUMBER: 131:98163
TITLE: Cloning of a Novel G-Protein-Coupled Receptor GPR 51 Resembling GABAB Receptors Expressed Predominantly in Nervous Tissues and Mapped Proximal to the Hereditary Sensory Neuropathy Type 1 Locus on Chromosome 9
AUTHOR(S): Ng, Gordon Y. K.; **McDonald, Terrence**; Bonnert, Tim; Rigby, Michael; Heavens, Robert; Whiting, Paul; Chateauneuf, Anne; Coulombe, Nathalie; Kargman, Stacia; Caskey, Thomas; Evans, Jilly; O'Neill, Gary P.; **Liu, Qingyun**
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Merck Frosst Center for Therapeutic Research, Kirkland, QC, H9H 3L1, Can.
SOURCE: Genomics (1999), 56(3), 288-295
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s hg51 (s) protein (s) coupled (s) receptor
L4 3 HG51 (S) PROTEIN (S) COUPLED (S) RECEPTOR

=> d l4 total ibib kwic

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:232346 CAPLUS
DOCUMENT NUMBER: 135:314242
TITLE: Characterization of a novel human opsin gene with wide tissue expression and identification of embedded and flanking genes on chromosome 1q43
AUTHOR(S): Halford, Stephanie; Freedman, Melanie S.; Bellingham, James; Inglis, Suzanne L.; Poopalasundaram, Subathra; Soni, Bobby G.; Foster, Russell G.; Hunt, David M.
CORPORATE SOURCE: Department of Molecular Genetics, Institute of Ophthalmology, University College London, London, EC1V 9EL, UK
SOURCE: Genomics (2001), 72(2), 203-208
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

IT 273191-92-7, G **protein-coupled receptor HG51** (human)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; characterization of a novel human opsin gene with wide tissue expression and identification of embedded and flanking genes on chromosome 1q43)

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:513802 CAPLUS
DOCUMENT NUMBER: 133:130801
TITLE: Cloning of a novel human G-protein-coupled receptor (GPCR)-17723 receptor cDNA and its therapeutic use
INVENTOR(S): Glucksmann, Maria Alexandra
PATENT ASSIGNEE(S): Millennium Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000043513	A1	20000727	WO 2000-US1592	20000121

W: AE, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-234923 A 19990121
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

IT 273191-92-7P, G **Protein-coupled receptor HG51** (human)
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
(amino acid sequence; cloning of novel human G-**protein-coupled receptor** (GPCR)-17723 **receptor** cDNA and its therapeutic use)

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:368396 CAPLUS
DOCUMENT NUMBER: 133:27864
TITLE: Human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant production and use in methods designed to identify agonists and/or antagonists
INVENTOR(S): Liu, Qingyun; McDonald, Terrence P.
PATENT ASSIGNEE(S): Merck & Co., Inc., USA
SOURCE: PCT Int. Appl., 68 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000031108	A1	20000602	WO 1999-US27305	19991118
EP 1133515	A1	20010919	EP 1999-962792	19991118

W: CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

PRIORITY APPLN. INFO.: US 1998-109717P P 19981124

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant production and use in methods designed to identify agonists and/or antagonists

AB The invention provides a cDNA mol. encoding a human G-**protein-coupled receptor, HG51**, as well as the **receptor** encoded by the cDNA mol. The invention also provides an expression vector (eukaryotic or prokaryotic) contg. HG51 cDNA mols. and host cells transformed with said vector, used for the recombinant prodn. of HG51. The invention further provides anti-HG51 antibodies. Still further, the invention provides methods for identifying substances that bind and/or modulate HG51, which include potential agonists and/or antagonists of HG51. The methods are cell based whereby an expression vector contg. polynucleotides encoding HG51 is transfected into a host cell, allowing for the recombinant prodn. of HG51 prior to addn. of the test substance. Finally, the invention provides the cDNA sequence, as well as the corresponding amino acid sequence of human HG51. The human **HG51 receptor** was shown to have sequence homol. to the rhodopsin subfamily of G **protein-coupled receptors**.

ST cDNA sequence human G **protein coupled receptor HG51**; recombinant prodn human G **protein coupled receptor HG51**; agonist human G **protein coupled receptor HG51** method identification; antagonist human G **protein coupled receptor HG51** method identification

IT G **protein-coupled receptors**
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
(**HG51**; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT Antibodies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(antibodies specific for human G-**protein-coupled receptor HG51**)

IT Cell membrane
(contains recombinant **HG51**; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT Genetic vectors
(eukaryotic or prokaryotic; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT Molecular cloning
Transformation, genetic
(human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT Ligands
RL: BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(of **HG51**; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT cDNA sequences
(of cDNA encoding human G **protein-coupled receptor HG51**)

IT **Protein** sequences
(of human G **protein-coupled receptor HG51**)

IT 273191-92-7P, G **Protein-coupled receptor HG51** (human)
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
(amino acid sequence; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT 273192-12-4D, subfragments are claimed
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; cDNA mol. encoding human G-**protein-coupled receptor HG51**, its sequence and use in recombinant prodn. of **HG51**)

IT 202544-98-7, 15: PN: WO0031108 SEQID: 3 unclaimed DNA 214908-88-0 214908-89-1 214908-90-4 273192-88-4, 3: PN: WO0031108 SEQID: 4 unclaimed DNA 273192-89-5, 4: PN: WO0031108 SEQID: 5 unclaimed DNA 273192-90-8, 5: PN: WO0031108 SEQID: 6 unclaimed DNA 273192-91-9, 6: PN: WO0031108 SEQID: 7 unclaimed DNA 273192-92-0, 7: PN: WO0031108 SEQID: 8 unclaimed DNA 273192-93-1, 8: PN: WO0031108 SEQID: 9 unclaimed DNA 273192-94-2, 9: PN: WO0031108 SEQID: 10 unclaimed DNA 290797-99-8
RL: PRP (Properties)
(unclaimed nucleotide sequence; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

IT 93050-34-1, Rhodopsin (human **protein** moiety reduced)
RL: PRP (Properties)
(unclaimed **protein** sequence; human G **protein-coupled receptor HG51**, its sequence, cDNA encoding it, recombinant prodn. and use in methods designed to identify agonists and/or antagonists)

09831765Results

SEQ ID NO: 1

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1470.4	95.7	2533	9	AF303588	AF303588 Homo sapi
	2	1380.8	89.8	2110	9	AF140242	AF140242 Homo sapi
	3	943.6	61.4	1737	10	AF140241	AF140241 Mus muscu
c	4	515.4	33.5	71872	9	AL133390	AL133390 Human DNA
c	5	424	27.6	5024	6	AX281720	AX281720 Sequence
c	6	422.4	27.5	5000	6	A68713	A68713 Sequence 5
c	7	422.4	27.5	5000	6	AR106624	AR106624 Sequence
c	8	422.4	27.5	5000	9	AF056032	AF056032 Homo sapi
	9	400.4	26.1	449	6	AX013137	AX013137 Sequence
	10	358	23.3	512	6	AX062411	AX062411 Sequence
c	11	317.2	20.6	8303	6	AX345325	AX345325 Sequence
	12	299.4	19.5	8303	6	AX345324	AX345324 Sequence

RESULT 1
AF303588
LOCUS AF303588 2533 bp mRNA linear PRI 17-APR-2001
DEFINITION Homo sapiens panopsin (OPN3) mRNA, complete cds.
ACCESSION AF303588
VERSION AF303588.1 GI:13649589
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2533)
AUTHORS Halford,S., Freedman,M.S., Bellingham,J., Inglis,S.L., Poopalasundaram,S., Soni,B.G., Foster,R.G. and Hunt,D.M.
TITLE Characterization of a novel human opsin gene with wide tissue expression and identification of embedded and flanking genes on chromosome 1q43
JOURNAL Genomics 72 (2), 203-208 (2001)
MEDLINE 21295039
REFERENCE 2 (bases 1 to 2533)
AUTHORS Halford,S., Bellingham,J., Freedman,M.S., Inglis,S.L., Poopalasundaram,S., Foster,R. and Hunt,D.M.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2000) Molecular Genetics, Institute of Ophthalmology, 11-43 Bath Street, London EC1V 9EL, UK
FEATURES Location/Qualifiers
source 1. .2533
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q43"
gene 1. .2533
/gene="OPN3"
CDS 103. .1311
/gene="OPN3"
/note="multiple tissue opsin"
/codon_start=1
/product="panopsin"
/protein_id="AAK37447.1"
/db_xref="GI:13649590"
/translation="MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERL
ALLLGSIGLLGVGNNLLVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSC
LRNGWVWDTVGCVWDGFSGSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITY
IWLYSLAWAGAPLLGWNRYILDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVI
AHCYGHILYSIRMLRCVEDLQTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICF
LVVNGHGHLVTPTISIVSYLFAKSNTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRP
AKDLPAAGSEMQIRPIVMSQKDGDRPKKKVTFNSSSIIFIITSDESLSVDDSDKTNGS
KVDVIQVRPL"

BASE COUNT 640 a 592 c 567 g 734 t
ORIGIN

Query Match 95.7%; Score 1470.4; DB 9; Length 2533;
Best Local Similarity 99.6%; Pred. No. 7.8e-229;
Matches 1474; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy      58 cagagcaggcggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgc 117
           | ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CGGACGCGTGGGCGGAGCCCCAGCCCCACCCAGTGCGGAGCGCGCCGCGAGCCCCGCCGC 60

Qy     118 aagctgagcgcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgc 177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGCTGAGCGCCTCCGCCCGCCAGGCGCGCCGGCGCCGGGCCATGTACTCGGGGAACCGC 120

Qy     178 agcggcggccacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccg 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCGGCGGCCACGGCTACTGGGACGGCGGCGGGGCCGCGGGCGCTGAGGGGCCGGCGCCG 180

Qy     238 gcggggacactgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctg 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCGGGGACACTGAGCCCCGCGCCCCTCTTCAGCCCCGGCACCTACGAGCGCCTGGCGCTG 240

Qy     298 ctgctgggctccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctac 357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTGGGCTCCATTGGGCTGCTGGGCGTCGGCAACAACCTGCTGGTGCTCGTCCTCTAC 300

Qy     358 tacaagttccagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagc 417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TACAAGTTCCAGCGGCTCCGCACTCCCACTCACCTCCTCCTGGTCAACATCAGCCTCAGC 360

Qy     418 gacctgctggtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggc 477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACCTGCTGGTGTCCCTCTTCGGGGTCACCTTTACCTTCGTGTCCTGCCTGAGGAACGGC 420

Qy     478 tgggtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggatt 537
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGGGTGTGGGACACCGTGGGCTGCGTGTGGGACGGGTTTAGCGGCAGCCTCTTCGGGATT 480

Qy     538 gtttccattgccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgcc 597
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GTTTCCATTGCCACCCTAACCGTGCTGGCCTATGAACGTTACATTCGCGTGGTCCATGCC 540

Qy     598 agagtgatcaatttttcctgggcctggagggccattacctacatctggctctactcactg 657
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGAGTGATCAATTTTTCCTGGGCCTGGAGGGCCATTACCTACATCTGGCTCTACTCACTG 600

Qy     658 gcgtgggcaggagcacctctcctgggatggaacaggtacatcctggacgtacacggacta 717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTGGGCAGGAGCACCTCTCCTGGGATGGAACAGGTACATCCTGGACGTACACGGACTA 660

Qy     718 ggctgcactgtggactggaaatccaaggatgccaacgattcctcctttgtgcttttctta 777
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GGCTGCACTGTGGACTGGAAATCCAAGGATGCCAACGATTCCTCCTTTGTGCTTTTCTTA 720

Qy     778 tttcttggctgcctggtggtgcccctgggtgtcatagcccattgctatggccatattcta 837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTCTTGGCTGCCTGGTGGTGCCCCTGGGTGTCATAGCCCATTGCTATGGCCATATTCTA 780

Qy     838 tattccattcgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagatt 897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TATTCCATTCGAATGCTTCGTTGTGTGGAAGATCTTCAGACAATTCAAGTGATCAAGATT 840

Qy     898 ttaaaatatgaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtc 957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TTAAAATATGAAAAGAAACTGGCCAAAATGTGCTTTTTAATGATATTCACCTTCCTGGTC 900

Qy     958 tgttggatgccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtc 1017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TGTTGGATGCCTTATATCGTGATCTGCTTCTTGGTGGTTAATGGTCATGGTCACCTGGTC 960
```

```
Qy   1018 actccaacaatatctattgtttcgtacctctttgctaaatcgaacactgtatacaatcca 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACTCCAACAATATCTATTGTTTCGTACCTCTTTGCTAAATCGAACACTGTATACAATCCA 1020

Qy   1078 gtgatttatgtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctc 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GTGATTTATGTCTTCATGATCAGAAAGTTTCGAAGATCCCTTTTGCAGCTTCTGTGCCTC 1080

Qy   1138 cgactgctgaggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcag 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGACTGCTGAGGTGCCAGAGGCCTGCTAAAGACCTACCAGCAGCTGGAAGTGAAATGCAG 1140

Qy   1198 atcagacccattgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttc 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATCAGACCCATTGTGATGTCACAGAAAGATGGGGACAGGCCAAAGAAAAAAGTGACTTTC 1200

Qy   1258 aactcttcttccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagc 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACTCTTCTTCCATCATTTTTATCATCACCAGTGATGAATCACTGTCAGTTGACGACAGC 1260

Qy   1318 gacaaaaccaatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaaga 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACAAAACCAATGGGTCCAAAGTTGATGTAATCCAAGTTCGTCCTTTGTAGGAATGAAGA 1320

Qy   1378 atggcaacgaaagatggggccttaaattggatgccacttttggactttcatcataagaag 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGCAACGAAAGATGGGGCCTTAAATTGGATGCCACTTTTGGACTTTCATCATAAGAAG 1380

Qy   1438 tgtctggaatacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccg 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGTCTGGAATACCCGTTCTATGTAATATCAACAGAACCTTGTGGTCCAGCAGGAAATCCG 1440

Qy   1498 aattgcccatatgctcttgggcctcaggaagaggttgaac 1537
          |||||||||||||||||||||||||||||||||||||||
Db   1441 AATTGCCCATATGCTCTTGGGCCTCAGGAAGAGGTTGAAC 1480
```

```
RESULT   2
AF140242
LOCUS       AF140242                2110 bp    mRNA    linear   PRI 27-MAY-1999
DEFINITION  Homo sapiens encephalopsin mRNA, complete cds.
ACCESSION   AF140242
VERSION     AF140242.1  GI:4894951
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2110)
  AUTHORS   Blackshaw,S. and Snyder,S.H.
  TITLE     Encephalopsin: A novel mammalian extraretinal opsin discretely
            localized in the brain
  JOURNAL   J. Neurosci. 19 (10), 3681-3690 (1999)
  MEDLINE   99252448
   PUBMED   10234000
REFERENCE   2  (bases 1 to 2110)
  AUTHORS   Blackshaw,S. and Snyder,S.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1999) Genetics, Harvard Medical School, 200
            Longwood Ave., Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .2110
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             56. .1267
                     /note="extraretinal opsin"
                     /codon_start=1
                     /product="encephalopsin"
                     /protein_id="AAD32671.1"
                     /db_xref="GI:4894952"
```

/translation="MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERL
ALLLGSIGLLGVGNNLLVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSC
LRNGWVWDTVGCVWDGFSGSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITY
IWLYSLAWAGAPLLGWNRYILDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVI
AHCYGHILYSIRMLRCVEDLQTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICF
LVVNGHGHLVTPTISIVSYLFAKSNTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRP
AKDLPAAGSEMQIRPIVMSQKDGDRPKKKVTFNSSSIIFIITSDESLSVDDSDKTIGV
QSLMLIQVRPL"

BASE COUNT 522 a 516 c 480 g 592 t

ORIGIN

Query Match 89.8%; Score 1380.8; DB 9; Length 2110;
Best Local Similarity 98.3%; Pred. No. 2.6e-214;
Matches 1421; Conservative 0; Mismatches 12; Indels 13; Gaps 2;

```
Qy   105 cgagccccgccgcaagctgagcgcctccgcccgccaggcgcgccggcgccgggccatgta 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CGAGCCCCGCCGCAAGCTGAGCGCCTCCGCCCGCCAGGCGCGCCGGCGCCGGGCCATGTA 60

Qy   165 ctcggggaaccgcagcggcggccacggctactgggacggcggcggggccgcgggcgctga 224
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CTCGGGGAACCGCAGCGGCGGCCACGGCTACTGGGACGGCGGCGGGGCCGCGGGCGCTGA 120

Qy   225 ggggccggcgccggcggggacactgagccccgcgcccctcttcagccccggcacctacga 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGGCCGGCGCCGGCGGGGACACTGAGCCCCGCGCCCCTCTTCAGCCCCGGCACCTACGA 180

Qy   285 gcgcctggcgctgctgctgggctccattgggctgctgggcgtcggcaacaacctgctggt 344
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCGCCTGGCGCTGCTGCTGGGCTCCATTGGGCTGCTGGGCGTCGGCAACAACCTGCTGGT 240

Qy   345 gctcgtcctctactacaagttccagcggctccgcactcccactcacctcctcctggtcaa 404
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCTCGTCCTCTACTACAAGTTCCAGCGGCTCCGCACTCCCACTCACCTCCTCCTGGTCAA 300

Qy   405 catcagcctcagcgacctgctggtgtccctcttcggggtcacctttaccttcgtgtcctg 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CATCAGCCTCAGCGACCTGCTGGTGTCCCTCTTCGGGGTCACCTTTACCTTCGTGTCCTG 360

Qy   465 cctgaggaacggctgggtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcag 524
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTGAGGAACGGCTGGGTGTGGGACACCGTGGGCTGCGTGTGGGACGGGTTTAGCGGCAG 420

Qy   525 cctcttcgggattgtttccattgccaccctaaccgtgctggcctatgaacgttacattcg 584
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTCTTCGGGATTGTTTCCATTGCCACCCTAACCGTGCTGGCCTATGAACGTTACATTCG 480

Qy   585 cgtggtccatgccagagtgatcaatttttcctgggcctggagggccattacctacatctg 644
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CGTGGTCCATGCCAGAGTGATCAATTTTTCCTGGGCCTGGAGGGCCATTACCTACATCTG 540

Qy   645 gctctactcactggcgtgggcaggagcacctctcctgggatggaacaggtacatcctgga 704
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCTCTACTCACTGGCGTGGGCAGGAGCACCTCTCCTGGGATGGAACAGGTACATCCTGGA 600

Qy   705 cgtacacggactaggctgcactgtggactggaaatccaaggatgccaacgattcctcctt 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGTACACGGACTAGGCTGCACTGTGGACTGGAAATCCAAGGATGCCAACGATTCCTCCTT 660

Qy   765 tgtgcttttcttatttcttggctgcctggtggtgcccctgggtgtcatagcccattgcta 824
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGTGCTTTTCTTATTTCTTGGCTGCCTGGTGGTGCCCCTGGGTGTCATAGCCCATTGCTA 720

Qy   825 tggccatattctatattccattcgaatgcttcgttgtgtggaagatcttcagacaattca 884
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TGGCCATATTCTATATTCCATTCGAATGCTTCGTTGTGTGGAAGATCTTCAGACAATTCA 780

Qy   885 agtgatcaagattttaaaatatgaaaagaaactggccaaaatgtgctttttaatgatatt 944
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AGTGATCAAGATTTTAAAATATGAAAAGAAACTGGCCAAAATGTGCTTTTTAATGATATT 840
```

```
Qy     945 caccttcctggtctgttggatgccttatatcgtgatctgcttcttggtggttaatggtca 1004
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CACCTTCCTGGTCTGTTGGATGCCTTATATCGTGATCTGCTTCTTGGTGGTTAATGGTCA 900

Qy    1005 tggtcacctggtcactccaacaatatctattgtttcgtacctctttgctaaatcgaacac 1064
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TGGTCACCTGGTCACTCCAACAATATCTATTGTTTCGTACCTCTTTGCTAAATCGAACAC 960

Qy    1065 tgtatacaatccagtgatttatgtcttcatgatcagaaagtttcgaagatccctttgca 1124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TGTATACAATCCAGTGATTTATGTCTTCATGATCAGAAAGTTTCGAAGATCCCTTTTGCA 1020

Qy    1125 gcttctgtgcctccgactgctgaggtgccagaggcctgctaaagacctaccagcagctgg 1184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GCTTCTGTGCCTCCGACTGCTGAGGTGCCAGAGGCCTGCTAAAGACCTACCAGCAGCTGG 1080

Qy    1185 aagtgaaatgcagatcagacccattgtgatgtcacagaaagatggggacaggccaaagaa 1244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AAGTGAAATGCAGATCAGACCCATTGTGATGTCACAGAAAGATGGGGACAGGCCAAAGAA 1140

Qy    1245 aaaagtgactttcaactcttcttccatcatttttatcatcaccagtgatgaatcactgtc 1304
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAAAGTGACTTTCAACTCTTCTTCCATCATTTTTATCATCACCAGTGATGAATCACTGTC 1200

Qy    1305 agttgacgacagcgacaaaaccaatgggtccaaa---gttgatgtaatccaagttcgtcc 1361
           |||||||||||||||||||||| ||||  | ||    |     ||||||||||||||||
Db    1201 AGTTGACGACAGCGACAAAACCATTGGGGTCCAAAGTTTGATGTTAATCCAAGTTCGTCC 1260

Qy    1362 tttgtaggaatgaagaatggcaacgaaagatggggccttaaattggatgccacttttgga 1421
           |||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Db    1261 TTTGTAGGAATGAAGGATGGCAACGAAAGGTGGGGCCTTAAATTGGATGCCACTTTTGGA 1320

Qy    1422 ctttcatcat----------aagaagtgtctggaatacccgttctatgtaatatcaacag 1471
           ||||||||||          ||||||||||||||||||||||||||||||||||||||||
Db    1321 CTTTCATCATCCTCCTGAAGAAGAAGTGTCTGGAATACCCGTTCTATGTAATATCAACAG 1380

Qy    1472 aaccttgtggtccagcaggaaatccgaattgcccatatgctcttgggcctcaggaagagg 1531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AACCTTGTGGTCCAGCAGGAAATCCGAATTGCCCATATGCTCTTGGGCCTCAGGAAGAGG 1440

Qy    1532 ttgaac 1537
           ||||||
Db    1441 TTGAAC 1446
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1537	100.0	1537	21	AAA38861	Human G-protein co
2	1459	94.9	2144	21	AAA73212	Human 17723 recept
3	1373.2	89.3	2037	22	AAD19720	Dendritic cell (DC
4	1028	66.9	1697	22	AAF33051	Human secreted pro
5	687.8	44.7	1267	21	AAZ34604	Human receptor mol
6	644.4	41.9	1763	21	AAC69518	Human secreted pro
7	437	28.4	619	22	AAD19721	Dendritic cell (DC
c 8	435	28.3	12291	22	AAK79265	Human immune/haema
c 9	424	27.6	5024	24	AAS94874	Human DNA sequence
c 10	422.4	27.5	5000	19	AAV20609	Human kynurenine-3
11	400.4	26.1	449	20	AAZ42057	Human endometrium

```
AAA38861
ID   AAA38861 standard; cDNA; 1537 BP.
XX
AC   AAA38861;
XX
```

DT 31-AUG-2000 (first entry)
XX
DE Human G-protein coupled receptor, HG51, coding sequence.
XX
KW Human; G-protein coupled receptor; HG51; signal transduction;
KW rhodopsin receptor; obesity; type II diabetes;
KW inflammatory bowel disease; constipation; diarrhoea; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 160..1368
FT /*tag= a
FT /product= "Human HG51"
XX
PN WO200031108-A1.
XX
PD 02-JUN-2000.
XX
PF 18-NOV-1999; 99WO-US27305.
XX
PR 24-NOV-1998; 98US-0109717.
XX
PA (MERI) MERCK & CO INC.
XX
PI Liu Q, McDonald TP;
XX
DR WPI; 2000-400025/34.
DR P-PSDB; AAY98008.
XX
PT New DNA encoding human HG51 (a G-protein coupled receptor), useful in
PT chromosomal mapping studies for identifying the chromosomal locations
PT of the HG51 gene(s) -
XX
PS Claim 1; Fig 1; 68pp; English.
XX
CC G protein-coupled receptors (GPCR) are important in signal transduction
CC from the exterior to the interior of cells. Rhodopsin receptors are a
CC type of GPCR which comprise a chromophore-binding pocket which is
CC covalently linked by a protonated Schiff base to a Lys residue in
CC transmembrane domain 7. The present sequence is the coding sequence of
CC the human HG51 GPCR and is a member of the rhodopsin receptor family of
CC GPCRs. Due to the Lys residue and Schiff base present in HG51, it is
CC thought that the HG51 ligand may be a fatty-acid-like molecule. It is
CC also believed that agonists and antagonists of HG51 are useful for
CC treating various disorders such as obesity, type II diabetes,
CC inflammatory bowel disease, constipation or diarrhoea. In addition, the
CC present sequence may be used in gene therapy for the above mentioned
CC disorders.
XX
SQ Sequence 1537 BP; 320 A; 426 C; 421 G; 370 T; 0 other;

Query Match 100.0%; Score 1537; DB 21; Length 1537;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ggggccacgggggtgcgccggcgcgcggtagcgcgggcccctcagtgcacaatggccag 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggggccacgggggtgcgccggcgcgcggtagcgcgggcccctcagtgcacaatggccag 60

Qy     61 agcaggcggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgcaag 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 agcaggcggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgcaag 120

Qy    121 ctgagcgcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ctgagcgcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagc 180

Qy    181 ggcggccacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db     181 ggcggccacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcg 240

Qy     241 gggacactgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctg 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 gggacactgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctg 300

Qy     301 ctgggctccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactac 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ctgggctccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactac 360

Qy     361 aagttccagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgac 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 aagttccagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgac 420

Qy     421 ctgctggtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgg 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ctgctggtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgg 480

Qy     481 gtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtt 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 gtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtt 540

Qy     541 tccattgccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccaga 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 tccattgccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccaga 600

Qy     601 gtgatcaatttttcctgggcctggagggccattacctacatctggctctactcactggcg 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 gtgatcaatttttcctgggcctggagggccattacctacatctggctctactcactggcg 660

Qy     661 tgggcaggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggc 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 tgggcaggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggc 720

Qy     721 tgcactgtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttattt 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 tgcactgtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttattt 780

Qy     781 cttggctgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatat 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 cttggctgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatat 840

Qy     841 tccattcgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagatttta 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 tccattcgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagatttta 900

Qy     901 aaatatgaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgt 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 aaatatgaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgt 960

Qy     961 tggatgccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcact 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 tggatgccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcact 1020

Qy    1021 ccaacaatatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtg 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ccaacaatatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtg 1080

Qy    1081 atttatgtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctccga 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 atttatgtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctccga 1140

Qy    1141 ctgctgaggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatc 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ctgctgaggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatc 1200

Qy    1201 agacccattgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaac 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 agacccattgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaac 1260

Qy    1261 tcttcttccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgac 1320
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 tcttcttccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgac 1320

Qy    1321 aaaaccaatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatg 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 aaaaccaatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatg 1380

Qy    1381 gcaacgaaagatggggccttaaattggatgccacttttggactttcatcataagaagtgt 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 gcaacgaaagatggggccttaaattggatgccacttttggactttcatcataagaagtgt 1440

Qy    1441 ctggaatacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaat 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ctggaatacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaat 1500

Qy    1501 tgcccatatgctcttgggcctcaggaagaggttgaac 1537
              |||||||||||||||||||||||||||||||||||
Db    1501 tgcccatatgctcttgggcctcaggaagaggttgaac 1537
```

RESULT 2
AAA73212
ID AAA73212 standard; cDNA; 2144 BP.
XX
AC AAA73212;
XX
DT 05-DEC-2000 (first entry)
XX
DE Human 17723 receptor protein encoding cDNA SEQ ID NO:2.
XX
KW Human; 17723 receptor protein; chromosome 1q42-44; diagnosis; vaccine;
KW G-protein coupled receptor; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200043513-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-US01592.
XX
PR 21-JAN-1999; 99US-0234923.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA;
XX
DR WPI; 2000-476196/41.
DR P-PSDB; AAB12827.
XX
PT A G-protein-coupled receptor designated 17723 and the nucleic acids
PT that encode it, useful for preventing, diagnosing and treating disorder
PT associated with inappropriate expression of 17723 receptors -
XX
PS Claim 3; Page 72-73; 79pp; English.
XX
CC The present sequence encodes the human 17723 receptor protein (I), which
CC belongs to the superfamily of G-protein-coupled receptors. (I) and the
CC polynucleotide encoding it may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate 17723 receptor
CC expression. They may also be used to study the expression and function
CC of 17723 receptor polypeptides and their role in metabolism. The 17723
CC receptor polypeptides may be used as antigens in the production of
CC antibodies against 17723 receptors and in assays to identify modulators
CC (agonists and antagonists) of 17723 receptor expression and activity.
CC The anti-17723 receptor antibodies and 17723 receptor antagonists may be
CC used to down regulate 17723 receptor expression and activity. The
CC anti-17723 receptor antibodies may also be used as diagnostic agents for
CC detecting the presence of 17723 receptor polypeptides in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The 17723 receptor
CC protein has been mapped to chromosome 1q42-44.

XX
SQ Sequence 2144 BP; 525 A; 531 C; 496 G; 590 T; 2 other;

Query Match 94.9%; Score 1459; DB 21; Length 2144;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1470; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      67 cggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgcaagctgagc 126
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1 cggcggagccccag-cccacccagtgcggagcgcgccgcgagccccgccgcaagctgagc  59

Qy     127 gcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagcggcggc 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 gcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagcggcggc 119

Qy     187 cacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcggggaca 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 cacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcggggaca 179

Qy     247 ctgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctgctgggc 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 ctgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctgctgggc 239

Qy     307 tccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactacaagttc 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 tccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactacaagttc 299

Qy     367 cagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgacctgctg 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 cagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgacctgctg 359

Qy     427 gtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgggtgtgg 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 gtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgggtgtgg 419

Qy     487 gacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtttccatt 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 gacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtttccatt 479

Qy     547 gccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccagagtgatc 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 gccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccagagtgatc 539

Qy     607 aatttttcctgggcctggagggccattacctacatctggctctactcactggcgtgggca 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 aatttttcctgggcctggagggccattacctacatctggctctactcactggcgtgggca 599

Qy     667 ggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggctgcact 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 ggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggctgcact 659

Qy     727 gtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttatttcttggc 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 gtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttatttcttggc 719

Qy     787 tgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatattccatt 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 tgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatattccatt 779

Qy     847 cgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagattttaaaatat 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 cgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagattttaaaatat 839

Qy     907 gaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgttggatg 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 gaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgttggatg 899

Qy     967 ccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcactccaaca 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 ccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcactccaaca 959
```

```
Qy   1027 atatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtgatttat 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 atatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtgatttat 1019

Qy   1087 gtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctccgactgctg 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 gtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctccgactgctg 1079

Qy   1147 aggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatcagaccc 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 aggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatcagaccc 1139

Qy   1207 attgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaactcttct 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 attgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaactcttct 1199

Qy   1267 tccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgacaaaacc 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 tccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgacaaaacc 1259

Qy   1327 aatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatggcaacg 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 aatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatggcaacg 1319

Qy   1387 aaagatggggccttaaattggatgccacttttggactttcatcataagaagtgtctggaa 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 aaagatggggccttaaattggatgccacttttggactttcatcataagaagtgtctggaa 1379

Qy   1447 tacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaattgccca 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 tacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaattgccca 1439

Qy   1507 tatgctcttgggcctcaggaagaggttgaac 1537
          ||||||||||||||||||||||||||||||
Db   1440 tatgctcttgggcctcaggaagaggttgaac 1470
```

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	422.4	27.5	5000	3	US-09-147-522-5	Sequence 5, Appli
	2	107.6	7.0	3016	1	US-07-805-123C-1	Sequence 1, Appli
	3	107.6	7.0	3016	1	US-08-033-081B-1	Sequence 1, Appli
	4	78	5.1	1105	2	US-08-466-103A-15	Sequence 15, Appl
	5	73	4.7	1410	4	US-09-255-368-1	Sequence 1, Appli
	6	69.2	4.5	1420	1	US-08-358-171-1	Sequence 1, Appli
	7	69.2	4.5	1420	3	US-09-090-947-1	Sequence 1, Appli
	8	67.2	4.4	1293	4	US-09-255-368-7	Sequence 7, Appli
	9	67	4.4	1776	1	US-08-722-001-29	Sequence 29, Appl
	10	65.4	4.3	2140	1	US-08-334-698-1	Sequence 1, Appli
	11	65.4	4.3	2140	1	US-08-228-932-1	Sequence 1, Appli
	12	65.4	4.3	2140	1	US-08-468-939-1	Sequence 1, Appli

Result No.	Score	Query Match	Length	DB	ID	Description
1	660.8	43.0	789	10	BI818538	BI818538 603033059
2	644.8	42.0	770	10	BI260681	BI260681 602968193
3	609.8	39.7	909	10	BE894106	BE894106 601438234
4	580.8	37.8	736	10	BI086726	BI086726 602850078
5	577.2	37.6	835	10	BF970560	BF970560 602274056
6	575	37.4	850	10	BI757207	BI757207 603030709
7	565.4	36.8	748	10	BG252201	BG252201 602365072
8	515.8	33.6	741	10	BG564220	BG564220 602586010
9	467.8	30.4	788	10	BF977798	BF977798 602148633
10	461.8	30.0	784	10	BI758685	BI758685 603024224

11	426.8	27.8	631	9	BB640431	BB640431 BB640431
12	426	27.7	819	10	BI088684	BI088684 602851458
13	423	27.5	424	10	BM194008	BM194008 TCAAP1E64
14	406.8	26.5	742	10	BI257225	BI257225 602976885
15	398.4	25.9	615	10	BF132059	BF132059 601821062

SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2117	100.0	402	21	AAB12827	Human 17723 recept
2	2117	100.0	402	21	AAY98008	Human G-protein co
3	2105	99.4	402	22	AAE12070	Dendritic cell (DC
4	1063	50.2	199	22	AAB64743	Human secreted pro
5	756	35.7	147	21	AAY32195	Human receptor mol
6	664	31.4	163	22	AAE12071	Dendritic cell (DC
7	664	31.4	879	22	AAU31008	Novel human secret
8	572	27.0	123	20	AAY60172	Human endometrium
9	564	26.6	122	21	AAB38327	Human secreted pro
10	459.5	21.7	349	10	AAP90554	Bovine rhodopsin.
11	455	21.5	348	17	AAR93116	Rhodopsin. Homo s
12	451	21.3	348	21	AAY98009	Human rhodopsin re
13	449	21.2	348	14	AAR38483	Rhodopsin protein.
14	424	20.0	354	21	AAY57086	Rhodopsin amino ac
15	420.5	19.9	309	15	AAR48735	G-protein coupled
16	420.5	19.9	309	17	AAW02707	G-protein coupled

RESULT 1
AAB12827
ID AAB12827 standard; Protein; 402 AA.
XX
AC AAB12827;
XX
DT 05-DEC-2000 (first entry)
XX
DE Human 17723 receptor protein SEQ ID NO:1.
XX
KW Human; 17723 receptor protein; chromosome 1q42-44; diagnosis; vaccine;
KW G-protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200043513-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-US01592.
XX
PR 21-JAN-1999; 99US-0234923.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA;
XX
DR WPI; 2000-476196/41.
DR N-PSDB; AAA73212.
XX
PT A G-protein-coupled receptor designated 17723 and the nucleic acids
PT that encode it, useful for preventing, diagnosing and treating disorder
PT associated with inappropriate expression of 17723 receptors -
XX
PS Claim 1; Page 70-72; 79pp; English.
XX
CC The present sequence is the human 17723 receptor protein (I), which

CC belongs to the superfamily of G-protein-coupled receptors. (I) and the
CC polynucleotide encoding it may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate 17723 receptor
CC expression. They may also be used to study the expression and function
CC of 17723 receptor polypeptides and their role in metabolism. The 17723
CC receptor polypeptides may be used as antigens in the production of
CC antibodies against 17723 receptors and in assays to identify modulators
CC (agonists and antagonists) of 17723 receptor expression and activity.
CC The anti-17723 receptor antibodies and 17723 receptor antagonists may be
CC used to down regulate 17723 receptor expression and activity. The
CC anti-17723 receptor antibodies may also be used as diagnostic agents for
CC detecting the presence of 17723 receptor polypeptides in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The 17723 receptor
CC protein has been mapped to chromosome 1q42-44.
XX
SQ Sequence 402 AA;

Query Match 100.0%; Score 2117; DB 21; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.3e-222;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mysgnrsgghgywdgggaagaegpapagtlspaplfspgtyerlalllgsigllgvgnnl 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 lvlvlyykfqrlrtpthlllvnislsdllvslfgvtftfvsclrngwvwdtvgcvwdgfs 120

Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwnryi 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ldvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcvedlqt 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 iqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylfaks 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ntvynpviyvfmirkfrrsllqllclrllrcqrpakdlpaagsemqirpivmsqkdgdrp 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
           |||||||||||||||||||||||||||||||||||||||||||
Db     361 kkkvtfnsssiifiitsdeslsvddsdktngskvdviqvrpl 402
```

RESULT 2
AAY98008
ID AAY98008 standard; Protein; 402 AA.
XX
AC AAY98008;
XX
DT 31-AUG-2000 (first entry)
XX
DE Human G-protein coupled receptor, HG51.
XX
KW Human; G-protein coupled receptor; HG51; signal transduction;
KW rhodopsin receptor; obesity; type II diabetes;
KW inflammatory bowel disease; constipation; diarrhoea; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200031108-A1.
XX
PD 02-JUN-2000.
XX

PF 18-NOV-1999; 99WO-US27305.
XX
PR 24-NOV-1998; 98US-0109717.
XX
PA (MERI) MERCK & CO INC.
XX
PI Liu Q, McDonald TP;
XX
DR WPI; 2000-400025/34.
DR N-PSDB; AAA38861.
XX
PT New DNA encoding human HG51 (a G-protein coupled receptor), useful in
PT chromosomal mapping studies for identifying the chromosomal locations
PT of the HG51 gene(s) -
XX
PS Claim 23; Fig 2; 68pp; English.
XX
CC G protein-coupled receptors (GPCR) are important in signal transduction
CC from the exterior to the interior of cells. Rhodopsin receptors are a
CC type of GPCR which comprise a chromophore-binding pocket which is
CC covalently linked by a protonated Schiff base to a Lys residue in
CC transmembrane domain 7. The present sequence is the human HG51 GPCR and
CC is a member of the rhodopsin receptor family of GPCRs. Due to the Lys
CC residue and Schiff base present in HG51, it is thought that the HG51
CC ligand may be a fatty-acid-like molecule. It is also believed that
CC agonists and antagonists of HG51 are useful for treating various
CC disorders such as obesity, type II diabetes, inflammatory bowel disease,
CC constipation or diarrhoea. In addition, the coding sequence for the
CC present sequence may be used in gene therapy for the above mentioned
CC disorders.
XX
SQ Sequence 402 AA;

Query Match 100.0%; Score 2117; DB 21; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.3e-222;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mysgnrsgghgywdgggaagaegpapagtlspaplfspgtyerlalllgsigllgvgnnl 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 lvlvlyykfqrlrtpthlllvnislsdllvslfgvtftfvsclrngwvwdtvgcvwdgfs 120

Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwnryi 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ldvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcvedlqt 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 iqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylfaks 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ntvynpviyvfmirkfrrsllqllclrllrcqrpakdlpaagsemqirpivmsqkdgdrp 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
          |||||||||||||||||||||||||||||||||||||||||||
Db     361 kkkvtfnsssiifiitsdeslsvddsdktngskvdviqvrpl 402
```

RESULT 3
AAE12070
ID AAE12070 standard; Protein; 402 AA.
XX

AC AAE12070;
XX
DT 18-DEC-2001 (first entry)
XX
DE Dendritic cell (DC) DCEPR protein.
XX
KW Dendritic cell; DC; DCEPR protein; gene therapy; dermatological; vaccine;
KW atopic dermatitis; autoimmune disease; inflammatory skin disease; cancer;
KW immunosuppressive; AIDS; Acquired immune deficiency syndrome; cytostatic;
KW chromosomal identification; pharmaceutical; hypersensitivity; virucide;
KW transplant rejection; chronic inflammatory disease; anti-HIV.
XX
OS Unidentified.
XX
PN WO200172773-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-EP03542.
XX
PR 29-MAR-2000; 2000US-192934P.
PR 18-MAY-2000; 2000US-205020P.
PR 18-MAY-2000; 2000US-205026P.
PR 19-MAY-2000; 2000US-205767P.
PR 19-MAY-2000; 2000US-205769P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Werner G, Phares W, Jaritz M, Lapp H, Kalthoff FS;
XX
DR WPI; 2001-616466/71.
DR N-PSDB; AAD19720.
XX
PT New polypeptides for screening therapeutic agonists and antagonists
PT comprise dendritic cell polypeptides -
XX
PS Claim 2; Page 42; 52pp; English.
XX
CC The invention relates to dendritic cell. (DC) proteins and their
CC corresponding DNA molecules. A pharmaceutical composition comprising
CC agonist and antagonist of DC proteins are useful for treating abnormal
CC conditions related to both an excess of and insufficient level of
CC expression of DC gene, or related to both an excess of and insufficient
CC activity of DC protein. Soluble form of DC proteins are used as an active
CC ingredient in combination with pharmaceutical acceptable carriers.
CC DC genes and proteins are useful for treating chronic inflammatory
CC diseases, autoimmune diseases, transplant rejection crisis, including
CC inflammatory skin diseases such as contact hypersensitivity, atopic
CC dermatitis or virally-induced immune suppression such as AIDS and cancer.
CC DC protein is useful for inducing immunological response in a mammal, and
CC as immunogen to produce antibodies immunospecific for the polypeptide.
CC DC gene is useful in gene therapy. DC gene is also useful as a diagnostic
CC reagent, and for chromosomal identification. The present sequence is
CC dendritic cell (DC) DCEPR protein which is found to belong to the family
CC of G-protein coupled receptor protein.
XX
SQ Sequence 402 AA;

Query Match 99.4%; Score 2105; DB 22; Length 402;
Best Local Similarity 99.5%; Pred. No. 1.3e-220;
Matches 400; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
           ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       1 mysgnrsgghgywdgggaagakgpapagtlspaplfspgtyerlalllgsigllgvgnnl 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 lvlvlyykfqrlrtpthlllvnislsdllvslfgvtftfvsclrngwvwdtvgcvwdgfs 120
```

```
Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwnryi 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ldvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcvedlqt 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 iqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylfaks 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ntvynpviyvfmirkfrrsllqllclrllrcqrpakdlpaagsemqirpivmsqkdgdrp 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
           ||||||||||||| |||||||||||||||||||||||||||||
Db     361 kkkvtfnsssiifigtsdeslsvddsdktngskvdviqvrpl 402
```

RESULT 4
AAB64743
ID AAB64743 standard; Protein; 199 AA.
XX
AC AAB64743;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:137.
XX
KW Human; secreted protein; diagnosis; cytostatic; antirheumatic;
KW antiarthritic; dermalogical; cardiant; antiinflammatory; anti-ulcer;
KW gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; myocardial angiogenesis; Crohn's disease;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200077237-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US14928.
XX
PR 11-JUN-1999; 99US-0138633.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-071280/08.
XX
PT Nucleic acids encoding 49 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating diseases such as tumors,
PT rheumatoid arthritis, psoriasis and diabetic retinopathy -
XX
PS Disclosure; Page 503; 520pp; English.
XX
CC The polynucleotide sequences given in AAF33037 to AAF33085 encode the
CC human secreted proteins given in AAB64666 to AAB64714. AAB64715 to
CC AAB64771 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC cytostatic; antirheumatic; antiarthritic; dermalogical; cardiant;
CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides
CC and polypeptides can be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate polypeptide expression.

CC Disorders that may be treated or prevented include solid tumours,
CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial
CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate
CC the presence of similar nucleic acid sequences in samples, and therefore
CC which patients may be in need of restorative therapy. The polypeptides
CC may also be used as antigens in the production of antibodies against the
CC polypeptide and in assays to identify modulators (agonists and
CC antagonists) of polypeptide expression and activity. The anti-polypeptide
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 199 AA;

Query Match 50.2%; Score 1063; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 2e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    118 GFSGSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWN 177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gfsgslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwn 60

Qy    178 RYILDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVED 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ryildvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcved 120

Qy    238 LQTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLF 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 lqtiqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylf 180

Qy    298 AKSNTVYNPVIYVFMIRKF 316
          ||||||||||||||||||
Db    181 aksntvynpviyvfmirkf 199
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	451	21.3	348	2	US-08-390-000A-8	Sequence 8, Appli
2	444	21.0	348	4	US-08-430-286A-11	Sequence 11, Appl
3	420.5	19.9	309	1	US-08-118-270-56	Sequence 56, Appl
4	420.5	19.9	309	5	PCT-US93-08528-56	Sequence 56, Appl
5	354.5	16.7	297	1	US-08-118-270-58	Sequence 58, Appl
6	354.5	16.7	297	5	PCT-US93-08528-58	Sequence 58, Appl
7	341.5	16.1	305	1	US-08-118-270-59	Sequence 59, Appl
8	341.5	16.1	305	5	PCT-US93-08528-59	Sequence 59, Appl
9	338.5	16.0	297	1	US-08-118-270-57	Sequence 57, Appl
10	338.5	16.0	297	5	PCT-US93-08528-57	Sequence 57, Appl
11	309	14.6	391	1	US-07-816-283-2	Sequence 2, Appli
12	309	14.6	391	1	US-08-417-103-2	Sequence 2, Appli
13	309	14.6	391	1	US-08-417-103-14	Sequence 14, Appl
14	304	14.4	391	1	US-07-816-283-4	Sequence 4, Appli
15	304	14.4	391	1	US-08-417-103-4	Sequence 4, Appli

Result No.	Score	Query Match	Length	DB	ID	Description
1	477.5	22.6	349	1	JC5490	opsin, pineal glan
2	475	22.4	351	1	A55962	opsin, pineal glan
3	464	21.9	352	2	I50081	rhodopsin - green
4	458	21.6	348	1	OOBO	rhodopsin - bovine
5	456.5	21.6	348	1	JC4267	opsin - rabbit
6	455	21.5	348	1	S23398	rhodopsin - Chines
7	452.5	21.4	351	2	S29152	rhodopsin - chicke

8	451	21.3	348	1	OOHU	rhodopsin - human
9	451	21.3	354	1	S27231	rhodopsin - northe
10	450	21.3	348	1	A23665	opsin - mouse
11	448	21.2	354	1	I51200	rhodopsin - Africa

Result No.	Score	Query Match	Length	DB	ID	Description
1	2117	100.0	402	1	OPN3_HUMAN	Q9hly3 homo sapien
2	1862	88.0	400	1	OPN3_MOUSE	Q9wuk7 mus musculu
3	477.5	22.6	349	1	OPSP_COLLI	P51476 columba liv
4	475	22.4	351	1	OPSP_CHICK	P51475 gallus gall
5	468	22.1	352	1	OPSD_ALLMI	P52202 alligator m
6	466.5	22.0	444	1	OPSP_PETMA	O42490 petromyzon
7	464	21.9	352	1	OPSD_ANOCA	P41591 anolis caro
8	458	21.6	348	1	OPSD_BOVIN	P02699 bos taurus
9	456.5	21.6	348	1	OPSD_RABIT	P49912 oryctolagus
10	455	21.5	348	1	OPSD_CRIGR	P28681 cricetulus
11	455	21.5	348	1	OPSD_MACFA	Q28886 macaca fasc
12	455	21.5	354	1	OPSD_RANCA	P51470 rana catesb

```
RESULT   1
OPN3_HUMAN
ID   OPN3_HUMAN     STANDARD;      PRT;   402 AA.
AC   Q9H1Y3; Q9Y344;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Opsin 3 (Encephalopsin) (Panopsin).
GN   OPN3 OR ECPN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99252448; PubMed=10234000;
RA   Blackshaw S., Snyder S.H.;
RT   "Encephalopsin: a novel mammalian extraretinal opsin discretely
RT   localized in the brain.";
RL   J. Neurosci. 19:3681-3690(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21295039; PubMed=11401433;
RA   Halford S., Freedman M.S., Bellingham J., Inglis S.L.,
RA   Poopalasundaram S., Soni B.G., Foster R.G., Hunt D.M.;
RT   "Characterization of a novel human opsin gene with wide tissue
RT   expression and identification of embedded and flanking genes on
RT   chromosome 1q43.";
RL   Genomics 72:203-208(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Parker A.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May play a role in encephalic photoreception.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Strongly expressed in brain. Highly expressed
CC       in the preoptic area and paraventricular nucleus of the
CC       hypothalamus. Shows highly patterned expression in other regions
CC       of the brain, being enriched in selected regions of the cerebral
CC       cortex, cerebellar Purkinje cells, a subset of striatal neurons,
CC       selected thalamic nuclei, and a subset of interneurons in the
CC       ventral horn of the spinal cord.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       OPSIN SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
```

```
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF140242; AAD32671.1; -.
DR   EMBL; AF303588; AAK37447.1; -.
DR   EMBL; AL133390; CAC19785.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00238; OPSIN; 1.
KW   Photoreceptor; Retinal protein; Transmembrane; Lipoprotein; Palmitate;
KW   G-protein coupled receptor.
FT   DOMAIN        1     40       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     41     65       1 (POTENTIAL).
FT   DOMAIN       66     77       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78    102       2 (POTENTIAL).
FT   DOMAIN      103    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    118    137       3 (POTENTIAL).
FT   DOMAIN      138    153       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    154    177       4 (POTENTIAL).
FT   DOMAIN      178    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    229       5 (POTENTIAL).
FT   DOMAIN      230    255       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    256    279       6 (POTENTIAL).
FT   DOMAIN      280    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    312       7 (POTENTIAL).
FT   DOMAIN      313    402       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    114    188       BY SIMILARITY.
FT   BINDING     299    299       RETINAL CHROMOPHORE.
FT   LIPID       325    325       PALMITATE (BY SIMILARITY).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    390    396       NGSKVDV -> IGVQSLML (IN REF. 1).
SQ   SEQUENCE   402 AA;  44873 MW;  370F64C19F834A71 CRC64;


  Query Match             100.0%;  Score 2117;  DB 1;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 1e-136;
  Matches  402;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120

Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
           |||||||||||||||||||||||||||||||||||||||||||
```

Db 361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402

Result No.	Score	% Query Match	Length	DB	ID	Description
1	500.5	23.6	352	13	Q9W6K3	Q9w6k3 anolis caro
2	491.5	23.2	534	13	O57422	O57422 xenopus lae
3	484.5	22.9	346	13	Q9PUA9	Q9pua9 bufo japoni
4	480	22.7	357	13	Q9IBH2	Q9ibh2 phelsuma ma
5	473.5	22.4	377	13	Q9IB88	Q9ib88 brachydanio
6	473	22.3	543	13	Q90YK6	Q90yk6 gallus gall
7	458	21.6	348	6	Q95KU1	Q95ku1 felis silve
8	457.5	21.6	351	13	Q9IA36	Q9ia36 poephila gu
9	455.5	21.5	351	13	Q9W6S0	Q9w6s0 columba liv
10	455	21.5	363	13	Q98TH3	Q98th3 cynops pyrr
11	453.5	21.4	322	13	O57448	O57448 anas platyr

09831765Results

SEQ ID NO: 1

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1470.4	95.7	2533	9	AF303588	AF303588 Homo sapi
	2	1380.8	89.8	2110	9	AF140242	AF140242 Homo sapi
	3	943.6	61.4	1737	10	AF140241	AF140241 Mus muscu
c	4	515.4	33.5	71872	9	AL133390	AL133390 Human DNA
c	5	424	27.6	5024	6	AX281720	AX281720 Sequence
c	6	422.4	27.5	5000	6	A68713	A68713 Sequence 5
c	7	422.4	27.5	5000	6	AR106624	AR106624 Sequence
c	8	422.4	27.5	5000	9	AF056032	AF056032 Homo sapi
	9	400.4	26.1	449	6	AX013137	AX013137 Sequence
	10	358	23.3	512	6	AX062411	AX062411 Sequence
c	11	317.2	20.6	8303	6	AX345325	AX345325 Sequence
	12	299.4	19.5	8303	6	AX345324	AX345324 Sequence

RESULT 1
AF303588
LOCUS AF303588 2533 bp mRNA linear PRI 17-APR-2001
DEFINITION Homo sapiens panopsin (OPN3) mRNA, complete cds.
ACCESSION AF303588
VERSION AF303588.1 GI:13649589
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2533)
AUTHORS Halford,S., Freedman,M.S., Bellingham,J., Inglis,S.L., Poopalasundaram,S., Soni,B.G., Foster,R.G. and Hunt,D.M.
TITLE Characterization of a novel human opsin gene with wide tissue expression and identification of embedded and flanking genes on chromosome 1q43
JOURNAL Genomics 72 (2), 203-208 (2001)
MEDLINE 21295039
REFERENCE 2 (bases 1 to 2533)
AUTHORS Halford,S., Bellingham,J., Freedman,M.S., Inglis,S.L., Poopalasundaram,S., Foster,R. and Hunt,D.M.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2000) Molecular Genetics, Institute of Ophthalmology, 11-43 Bath Street, London EC1V 9EL, UK
FEATURES Location/Qualifiers
source 1. .2533
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q43"
gene 1. .2533
/gene="OPN3"
CDS 103. .1311
/gene="OPN3"
/note="multiple tissue opsin"
/codon_start=1
/product="panopsin"
/protein_id="AAK37447.1"
/db_xref="GI:13649590"
/translation="MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERL
ALLLGSIGLLGVGNNLLVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSC
LRNGWVWDTVGCVWDGFSGSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITY
IWLYSLAWAGAPLLGWNRYILDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVI
AHCYGHILYSIRMLRCVEDLQTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICF
LVVNGHGHLVTPTISIVSYLFAKSNTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRP
AKDLPAAGSEMQIRPIVMSQKDGDRPKKKVTFNSSSIIFIITSDESLSVDDSDKTNGS
KVDVIQVRPL"

BASE COUNT 640 a 592 c 567 g 734 t
ORIGIN

Query Match 95.7%; Score 1470.4; DB 9; Length 2533;
Best Local Similarity 99.6%; Pred. No. 7.8e-229;
Matches 1474; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy      58 cagagcaggcggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgc 117
           | ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CGGACGCGTGGGCGGAGCCCCAGCCCCACCCAGTGCGGAGCGCGCCGCGAGCCCCGCCGC 60

Qy     118 aagctgagcgcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgc 177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGCTGAGCGCCTCCGCCCGCCAGGCGCGCCGGCGCCGGGCCATGTACTCGGGGAACCGC 120

Qy     178 agcggcggccacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccg 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCGGCGGCCACGGCTACTGGGACGGCGGCGGGGCCGCGGGCGCTGAGGGGCCGGCGCCG 180

Qy     238 gcggggacactgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctg 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCGGGGACACTGAGCCCCGCGCCCCTCTTCAGCCCCGGCACCTACGAGCGCCTGGCGCTG 240

Qy     298 ctgctgggctccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctac 357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTGGGCTCCATTGGGCTGCTGGGCGTCGGCAACAACCTGCTGGTGCTCGTCCTCTAC 300

Qy     358 tacaagttccagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagc 417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TACAAGTTCCAGCGGCTCCGCACTCCCACTCACCTCCTCCTGGTCAACATCAGCCTCAGC 360

Qy     418 gacctgctggtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggc 477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACCTGCTGGTGTCCCTCTTCGGGGTCACCTTTACCTTCGTGTCCTGCCTGAGGAACGGC 420

Qy     478 tgggtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggatt 537
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGGGTGTGGGACACCGTGGGCTGCGTGTGGGACGGGTTTAGCGGCAGCCTCTTCGGGATT 480

Qy     538 gtttccattgccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgcc 597
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GTTTCCATTGCCACCCTAACCGTGCTGGCCTATGAACGTTACATTCGCGTGGTCCATGCC 540

Qy     598 agagtgatcaatttttcctgggcctggagggccattacctacatctggctctactcactg 657
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGAGTGATCAATTTTTCCTGGGCCTGGAGGGCCATTACCTACATCTGGCTCTACTCACTG 600

Qy     658 gcgtgggcaggagcacctctcctgggatggaacaggtacatcctggacgtacacggacta 717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTGGGCAGGAGCACCTCTCCTGGGATGGAACAGGTACATCCTGGACGTACACGGACTA 660

Qy     718 ggctgcactgtggactggaaatccaaggatgccaacgattcctccttttgtgcttttctta 777
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GGCTGCACTGTGGACTGGAAATCCAAGGATGCCAACGATTCCTCCTTTGTGCTTTTCTTA 720

Qy     778 tttcttggctgcctggtggtgcccctgggtgtcatagcccattgctatggccatattcta 837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTCTTGGCTGCCTGGTGGTGCCCCTGGGTGTCATAGCCCATTGCTATGGCCATATTCTA 780

Qy     838 tattccattcgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagatt 897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TATTCCATTCGAATGCTTCGTTGTGTGGAAGATCTTCAGACAATTCAAGTGATCAAGATT 840

Qy     898 ttaaaatatgaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtc 957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TTAAAATATGAAAAGAAACTGGCCAAAATGTGCTTTTTAATGATATTCACCTTCCTGGTC 900

Qy     958 tgttggatgccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtc 1017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TGTTGGATGCCTTATATCGTGATCTGCTTCTTGGTGGTTAATGGTCATGGTCACCTGGTC 960
```

```
Qy   1018 actccaacaatatctattgtttcgtacctctttgctaaatcgaacactgtatacaatcca 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACTCCAACAATATCTATTGTTTCGTACCTCTTTGCTAAATCGAACACTGTATACAATCCA 1020

Qy   1078 gtgatttatgtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctc 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GTGATTTATGTCTTCATGATCAGAAAGTTTCGAAGATCCCTTTTGCAGCTTCTGTGCCTC 1080

Qy   1138 cgactgctgaggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcag 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CGACTGCTGAGGTGCCAGAGGCCTGCTAAAGACCTACCAGCAGCTGGAAGTGAAATGCAG 1140

Qy   1198 atcagacccattgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttc 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATCAGACCCATTGTGATGTCACAGAAAGATGGGGACAGGCCAAAGAAAAAAGTGACTTTC 1200

Qy   1258 aactcttcttccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagc 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACTCTTCTTCCATCATTTTTATCATCACCAGTGATGAATCACTGTCAGTTGACGACAGC 1260

Qy   1318 gacaaaaccaatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaaga 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GACAAAACCAATGGGTCCAAAGTTGATGTAATCCAAGTTCGTCCTTTGTAGGAATGAAGA 1320

Qy   1378 atggcaacgaaagatggggccttaaattggatgccacttttggactttcatcataagaag 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGCAACGAAAGATGGGGCCTTAAATTGGATGCCACTTTTGGACTTTCATCATAAGAAG 1380

Qy   1438 tgtctggaatacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccg 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGTCTGGAATACCCGTTCTATGTAATATCAACAGAACCTTGTGGTCCAGCAGGAAATCCG 1440

Qy   1498 aattgcccatatgctcttgggcctcaggaagaggttgaac 1537
          |||||||||||||||||||||||||||||||||||||||
Db   1441 AATTGCCCATATGCTCTTGGGCCTCAGGAAGAGGTTGAAC 1480
```

```
RESULT   2
AF140242
LOCUS       AF140242                2110 bp    mRNA    linear   PRI 27-MAY-1999
DEFINITION  Homo sapiens encephalopsin mRNA, complete cds.
ACCESSION   AF140242
VERSION     AF140242.1  GI:4894951
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2110)
  AUTHORS   Blackshaw,S. and Snyder,S.H.
  TITLE     Encephalopsin: A novel mammalian extraretinal opsin discretely
            localized in the brain
  JOURNAL   J. Neurosci. 19 (10), 3681-3690 (1999)
  MEDLINE   99252448
   PUBMED   10234000
REFERENCE   2  (bases 1 to 2110)
  AUTHORS   Blackshaw,S. and Snyder,S.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1999) Genetics, Harvard Medical School, 200
            Longwood Ave., Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .2110
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             56. .1267
                     /note="extraretinal opsin"
                     /codon_start=1
                     /product="encephalopsin"
                     /protein_id="AAD32671.1"
                     /db_xref="GI:4894952"
```

/translation="MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERL
ALLLGSIGLLGVGNNLLVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSC
LRNGWVWDTVGCVWDGFSGSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITY
IWLYSLAWAGAPLLGWNRYILDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVI
AHCYGHILYSIRMLRCVEDLQTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICF
LVVNGHGHLVTPTISIVSYLFAKSNTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRP
AKDLPAAGSEMQIRPIVMSQKDGDRPKKKVTFNSSSIIFIITSDESLSVDDSDKTIGV
QSLMLIQVRPL"

BASE COUNT 522 a 516 c 480 g 592 t

ORIGIN

Query Match 89.8%; Score 1380.8; DB 9; Length 2110;
Best Local Similarity 98.3%; Pred. No. 2.6e-214;
Matches 1421; Conservative 0; Mismatches 12; Indels 13; Gaps 2;

```
Qy   105 cgagccccgccgcaagctgagcgcctccgcccgccaggcgcgccggcgccgggccatgta 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CGAGCCCCGCCGCAAGCTGAGCGCCTCCGCCCGCCAGGCGCGCCGGCGCCGGGCCATGTA 60

Qy   165 ctcggggaaccgcagcggcggccacggctactgggacggcggcggggccgcgggcgctga 224
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CTCGGGGAACCGCAGCGGCGGCCACGGCTACTGGGACGGCGGCGGGGCCGCGGGCGCTGA 120

Qy   225 ggggccggcgccggcggggacactgagccccgcgcccctcttcagccccggcacctacga 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGGCCGGCGCCGGCGGGGACACTGAGCCCCGCGCCCCTCTTCAGCCCCGGCACCTACGA 180

Qy   285 gcgcctggcgctgctgctgggctccattgggctgctgggcgtcggcaacaacctgctggt 344
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCGCCTGGCGCTGCTGCTGGGCTCCATTGGGCTGCTGGGCGTCGGCAACAACCTGCTGGT 240

Qy   345 gctcgtcctctactacaagttccagcggctccgcactcccactcacctcctcctggtcaa 404
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCTCGTCCTCTACTACAAGTTCCAGCGGCTCCGCACTCCCACTCACCTCCTCCTGGTCAA 300

Qy   405 catcagcctcagcgacctgctggtgtccctcttcggggtcacctttaccttcgtgtcctg 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CATCAGCCTCAGCGACCTGCTGGTGTCCCTCTTCGGGGTCACCTTTACCTTCGTGTCCTG 360

Qy   465 cctgaggaacggctgggtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcag 524
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTGAGGAACGGCTGGGTGTGGGACACCGTGGGCTGCGTGTGGGACGGGTTTAGCGGCAG 420

Qy   525 cctcttcgggattgtttccattgccaccctaaccgtgctggcctatgaacgttacattcg 584
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTCTTCGGGATTGTTTCCATTGCCACCCTAACCGTGCTGGCCTATGAACGTTACATTCG 480

Qy   585 cgtggtccatgccagagtgatcaatttttcctgggcctggagggccattacctacatctg 644
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CGTGGTCCATGCCAGAGTGATCAATTTTTCCTGGGCCTGGAGGGCCATTACCTACATCTG 540

Qy   645 gctctactcactggcgtgggcaggagcacctctcctgggatggaacaggtacatcctgga 704
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCTCTACTCACTGGCGTGGGCAGGAGCACCTCTCCTGGGATGGAACAGGTACATCCTGGA 600

Qy   705 cgtacacggactaggctgcactgtggactggaaatccaaggatgccaacgattcctcctt 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGTACACGGACTAGGCTGCACTGTGGACTGGAAATCCAAGGATGCCAACGATTCCTCCTT 660

Qy   765 tgtgcttttcttatttcttggctgcctggtggtgcccctgggtgtcatagcccattgcta 824
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGTGCTTTTCTTATTTCTTGGCTGCCTGGTGGTGCCCCTGGGTGTCATAGCCCATTGCTA 720

Qy   825 tggccatattctatattccattcgaatgcttcgttgtgtggaagatcttcagacaattca 884
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TGGCCATATTCTATATTCCATTCGAATGCTTCGTTGTGTGGAAGATCTTCAGACAATTCA 780

Qy   885 agtgatcaagattttaaaatatgaaaagaaactggccaaaatgtgctttttaatgatatt 944
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AGTGATCAAGATTTTAAAATATGAAAAGAAACTGGCCAAAATGTGCTTTTTAATGATATT 840
```

```
Qy     945 caccttcctggtctgttggatgccttatatcgtgatctgcttcttggtggttaatggtca 1004
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CACCTTCCTGGTCTGTTGGATGCCTTATATCGTGATCTGCTTCTTGGTGGTTAATGGTCA 900

Qy    1005 tggtcacctggtcactccaacaatatctattgtttcgtacctctttgctaaatcgaacac 1064
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TGGTCACCTGGTCACTCCAACAATATCTATTGTTTCGTACCTCTTTGCTAAATCGAACAC 960

Qy    1065 tgtatacaatccagtgatttatgtcttcatgatcagaaagtttcgaagatccctttgca 1124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TGTATACAATCCAGTGATTTATGTCTTCATGATCAGAAAGTTTCGAAGATCCCTTTTGCA 1020

Qy    1125 gcttctgtgcctccgactgctgaggtgccagaggcctgctaaagacctaccagcagctgg 1184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GCTTCTGTGCCTCCGACTGCTGAGGTGCCAGAGGCCTGCTAAAGACCTACCAGCAGCTGG 1080

Qy    1185 aagtgaaatgcagatcagacccattgtgatgtcacagaaagatggggacaggccaaagaa 1244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AAGTGAAATGCAGATCAGACCCATTGTGATGTCACAGAAAGATGGGGACAGGCCAAAGAA 1140

Qy    1245 aaaagtgactttcaactcttcttccatcatttttatcatcaccagtgatgaatcactgtc 1304
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAAAGTGACTTTCAACTCTTCTTCCATCATTTTTATCATCACCAGTGATGAATCACTGTC 1200

Qy    1305 agttgacgacagcgacaaaaccaatgggtccaaa---gttgatgtaatccaagttcgtcc 1361
           |||||||||||||||||||||| ||||  | ||    |     ||||||||||||||||
Db    1201 AGTTGACGACAGCGACAAAACCATTGGGGTCCAAAGTTTGATGTTAATCCAAGTTCGTCC 1260

Qy    1362 tttgtaggaatgaagaatggcaacgaaagatggggccttaaattggatgccacttttgga 1421
           ||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Db    1261 TTTGTAGGAATGAAGGATGGCAACGAAAGGTGGGGCCTTAAATTGGATGCCACTTTTGGA 1320

Qy    1422 ctttcatcat----------aagaagtgtctggaatacccgttctatgtaatatcaacag 1471
           ||||||||||          ||||||||||||||||||||||||||||||||||||||||
Db    1321 CTTTCATCATCCTCCTGAAGAAGAAGTGTCTGGAATACCCGTTCTATGTAATATCAACAG 1380

Qy    1472 aaccttgtggtccagcaggaaatccgaattgcccatatgctcttgggcctcaggaagagg 1531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AACCTTGTGGTCCAGCAGGAAATCCGAATTGCCCATATGCTCTTGGGCCTCAGGAAGAGG 1440

Qy    1532 ttgaac 1537
           ||||||
Db    1441 TTGAAC 1446
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1537	100.0	1537	21	AAA38861	Human G-protein co
2	1459	94.9	2144	21	AAA73212	Human 17723 recept
3	1373.2	89.3	2037	22	AAD19720	Dendritic cell (DC
4	1028	66.9	1697	22	AAF33051	Human secreted pro
5	687.8	44.7	1267	21	AAZ34604	Human receptor mol
6	644.4	41.9	1763	21	AAC69518	Human secreted pro
7	437	28.4	619	22	AAD19721	Dendritic cell (DC
c 8	435	28.3	12291	22	AAK79265	Human immune/haema
c 9	424	27.6	5024	24	AAS94874	Human DNA sequence
c 10	422.4	27.5	5000	19	AAV20609	Human kynurenine-3
11	400.4	26.1	449	20	AAZ42057	Human endometrium

```
AAA38861
ID   AAA38861 standard; cDNA; 1537 BP.
XX
AC   AAA38861;
XX
```

DT 31-AUG-2000 (first entry)
XX
DE Human G-protein coupled receptor, HG51, coding sequence.
XX
KW Human; G-protein coupled receptor; HG51; signal transduction;
KW rhodopsin receptor; obesity; type II diabetes;
KW inflammatory bowel disease; constipation; diarrhoea; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 160..1368
FT /*tag= a
FT /product= "Human HG51"
XX
PN WO200031108-A1.
XX
PD 02-JUN-2000.
XX
PF 18-NOV-1999; 99WO-US27305.
XX
PR 24-NOV-1998; 98US-0109717.
XX
PA (MERI) MERCK & CO INC.
XX
PI Liu Q, McDonald TP;
XX
DR WPI; 2000-400025/34.
DR P-PSDB; AAY98008.
XX
PT New DNA encoding human HG51 (a G-protein coupled receptor), useful in
PT chromosomal mapping studies for identifying the chromosomal locations
PT of the HG51 gene(s) -
XX
PS Claim 1; Fig 1; 68pp; English.
XX
CC G protein-coupled receptors (GPCR) are important in signal transduction
CC from the exterior to the interior of cells. Rhodopsin receptors are a
CC type of GPCR which comprise a chromophore-binding pocket which is
CC covalently linked by a protonated Schiff base to a Lys residue in
CC transmembrane domain 7. The present sequence is the coding sequence of
CC the human HG51 GPCR and is a member of the rhodopsin receptor family of
CC GPCRs. Due to the Lys residue and Schiff base present in HG51, it is
CC thought that the HG51 ligand may be a fatty-acid-like molecule. It is
CC also believed that agonists and antagonists of HG51 are useful for
CC treating various disorders such as obesity, type II diabetes,
CC inflammatory bowel disease, constipation or diarrhoea. In addition, the
CC present sequence may be used in gene therapy for the above mentioned
CC disorders.
XX
SQ Sequence 1537 BP; 320 A; 426 C; 421 G; 370 T; 0 other;

Query Match 100.0%; Score 1537; DB 21; Length 1537;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ggggccacgggggtgcgccggcgcgcggtagcgcgggcccctcagtgcacaatggccag 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ggggccacgggggtgcgccggcgcgcggtagcgcgggcccctcagtgcacaatggccag 60

Qy      61 agcaggcggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgcaag 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 agcaggcggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgcaag 120

Qy     121 ctgagcgcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ctgagcgcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagc 180

Qy     181 ggcggccacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcg 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db     181 ggcggccacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcg 240

Qy     241 gggacactgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctg 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 gggacactgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctg 300

Qy     301 ctgggctccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactac 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ctgggctccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactac 360

Qy     361 aagttccagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgac 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 aagttccagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgac 420

Qy     421 ctgctggtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgg 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ctgctggtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgg 480

Qy     481 gtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtt 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 gtgtgggacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtt 540

Qy     541 tccattgccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccaga 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 tccattgccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccaga 600

Qy     601 gtgatcaatttttcctgggcctggagggccattacctacatctggctctactcactggcg 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 gtgatcaatttttcctgggcctggagggccattacctacatctggctctactcactggcg 660

Qy     661 tgggcaggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggc 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 tgggcaggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggc 720

Qy     721 tgcactgtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttattt 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 tgcactgtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttattt 780

Qy     781 cttggctgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatat 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 cttggctgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatat 840

Qy     841 tccattcgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagatttta 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 tccattcgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagatttta 900

Qy     901 aaatatgaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgt 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 aaatatgaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgt 960

Qy     961 tggatgccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcact 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 tggatgccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcact 1020

Qy    1021 ccaacaatatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtg 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ccaacaatatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtg 1080

Qy    1081 atttatgtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctccga 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 atttatgtcttcatgatcagaaagtttcgaagatccctttgcagcttctgtgcctccga 1140

Qy    1141 ctgctgaggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatc 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ctgctgaggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatc 1200

Qy    1201 agacccattgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaac 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 agacccattgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaac 1260

Qy    1261 tcttcttccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgac 1320
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 tcttcttccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgac 1320

Qy   1321 aaaaccaatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aaaaccaatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatg 1380

Qy   1381 gcaacgaaagatggggccttaaattggatgccacttttggactttcatcataagaagtgt 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 gcaacgaaagatggggccttaaattggatgccacttttggactttcatcataagaagtgt 1440

Qy   1441 ctggaatacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaat 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ctggaatacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaat 1500

Qy   1501 tgcccatatgctcttgggcctcaggaagaggttgaac 1537
          |||||||||||||||||||||||||||||||||||
Db   1501 tgcccatatgctcttgggcctcaggaagaggttgaac 1537
```

RESULT 2
AAA73212
ID AAA73212 standard; cDNA; 2144 BP.
XX
AC AAA73212;
XX
DT 05-DEC-2000 (first entry)
XX
DE Human 17723 receptor protein encoding cDNA SEQ ID NO:2.
XX
KW Human; 17723 receptor protein; chromosome 1q42-44; diagnosis; vaccine;
KW G-protein coupled receptor; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200043513-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-US01592.
XX
PR 21-JAN-1999; 99US-0234923.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA;
XX
DR WPI; 2000-476196/41.
DR P-PSDB; AAB12827.
XX
PT A G-protein-coupled receptor designated 17723 and the nucleic acids
PT that encode it, useful for preventing, diagnosing and treating disorder
PT associated with inappropriate expression of 17723 receptors -
XX
PS Claim 3; Page 72-73; 79pp; English.
XX
CC The present sequence encodes the human 17723 receptor protein (I), which
CC belongs to the superfamily of G-protein-coupled receptors. (I) and the
CC polynucleotide encoding it may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate 17723 receptor
CC expression. They may also be used to study the expression and function
CC of 17723 receptor polypeptides and their role in metabolism. The 17723
CC receptor polypeptides may be used as antigens in the production of
CC antibodies against 17723 receptors and in assays to identify modulators
CC (agonists and antagonists) of 17723 receptor expression and activity.
CC The anti-17723 receptor antibodies and 17723 receptor antagonists may be
CC used to down regulate 17723 receptor expression and activity. The
CC anti-17723 receptor antibodies may also be used as diagnostic agents for
CC detecting the presence of 17723 receptor polypeptides in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The 17723 receptor
CC protein has been mapped to chromosome 1q42-44.

XX
SQ Sequence 2144 BP; 525 A; 531 C; 496 G; 590 T; 2 other;

Query Match 94.9%; Score 1459; DB 21; Length 2144;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1470; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      67 cggcggagccccagccccacccagtgcggagcgcgccgcgagccccgccgcaagctgagc 126
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1 cggcggagccccag-cccacccagtgcggagcgcgccgcgagccccgccgcaagctgagc 59

Qy     127 gcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagcggcggc 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 gcctccgcccgccaggcgcgccggcgccgggccatgtactcggggaaccgcagcggcggc 119

Qy     187 cacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcggggaca 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 cacggctactgggacggcggcggggccgcgggcgctgaggggccggcgccggcggggaca 179

Qy     247 ctgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctgctgggc 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 ctgagccccgcgcccctcttcagccccggcacctacgagcgcctggcgctgctgctgggc 239

Qy     307 tccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactacaagttc 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 tccattgggctgctgggcgtcggcaacaacctgctggtgctcgtcctctactacaagttc 299

Qy     367 cagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgacctgctg 426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 cagcggctccgcactcccactcacctcctcctggtcaacatcagcctcagcgacctgctg 359

Qy     427 gtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgggtgtgg 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 gtgtccctcttcggggtcacctttaccttcgtgtcctgcctgaggaacggctgggtgtgg 419

Qy     487 gacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtttccatt 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 gacaccgtgggctgcgtgtgggacgggtttagcggcagcctcttcgggattgtttccatt 479

Qy     547 gccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccagagtgatc 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 gccaccctaaccgtgctggcctatgaacgttacattcgcgtggtccatgccagagtgatc 539

Qy     607 aatttttcctgggcctggagggccattacctacatctggctctactcactggcgtgggca 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 aatttttcctgggcctggagggccattacctacatctggctctactcactggcgtgggca 599

Qy     667 ggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggctgcact 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 ggagcacctctcctgggatggaacaggtacatcctggacgtacacggactaggctgcact 659

Qy     727 gtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttatttcttggc 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 gtggactggaaatccaaggatgccaacgattcctcctttgtgcttttcttatttcttggc 719

Qy     787 tgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatattccatt 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 tgcctggtggtgcccctgggtgtcatagcccattgctatggccatattctatattccatt 779

Qy     847 cgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagattttaaaatat 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 cgaatgcttcgttgtgtggaagatcttcagacaattcaagtgatcaagattttaaaatat 839

Qy     907 gaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgttggatg 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 gaaaagaaactggccaaaatgtgctttttaatgatattcaccttcctggtctgttggatg 899

Qy     967 ccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcactccaaca 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 ccttatatcgtgatctgcttcttggtggttaatggtcatggtcacctggtcactccaaca 959
```

```
Qy   1027 atatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtgatttat 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 atatctattgtttcgtacctctttgctaaatcgaacactgtatacaatccagtgatttat 1019

Qy   1087 gtcttcatgatcagaaagtttcgaagatccctttttgcagcttctgtgcctccgactgctg 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 gtcttcatgatcagaaagtttcgaagatccctttttgcagcttctgtgcctccgactgctg 1079

Qy   1147 aggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatcagaccc 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 aggtgccagaggcctgctaaagacctaccagcagctggaagtgaaatgcagatcagaccc 1139

Qy   1207 attgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaactcttct 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 attgtgatgtcacagaaagatggggacaggccaaagaaaaaagtgactttcaactcttct 1199

Qy   1267 tccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgacaaaacc 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 tccatcatttttatcatcaccagtgatgaatcactgtcagttgacgacagcgacaaaacc 1259

Qy   1327 aatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatggcaacg 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 aatgggtccaaagttgatgtaatccaagttcgtcctttgtaggaatgaagaatggcaacg 1319

Qy   1387 aaagatggggccttaaattggatgccacttttggactttcatcataagaagtgtctggaa 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 aaagatggggccttaaattggatgccacttttggactttcatcataagaagtgtctggaa 1379

Qy   1447 tacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaattgccca 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 tacccgttctatgtaatatcaacagaaccttgtggtccagcaggaaatccgaattgccca 1439

Qy   1507 tatgctcttgggcctcaggaagaggttgaac 1537
          |||||||||||||||||||||||||||||
Db   1440 tatgctcttgggcctcaggaagaggttgaac 1470
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	422.4	27.5	5000	3	US-09-147-522-5	Sequence 5, Appli
2	107.6	7.0	3016	1	US-07-805-123C-1	Sequence 1, Appli
3	107.6	7.0	3016	1	US-08-033-081B-1	Sequence 1, Appli
4	78	5.1	1105	2	US-08-466-103A-15	Sequence 15, Appl
5	73	4.7	1410	4	US-09-255-368-1	Sequence 1, Appli
6	69.2	4.5	1420	1	US-08-358-171-1	Sequence 1, Appli
7	69.2	4.5	1420	3	US-09-090-947-1	Sequence 1, Appli
8	67.2	4.4	1293	4	US-09-255-368-7	Sequence 7, Appli
9	67	4.4	1776	1	US-08-722-001-29	Sequence 29, Appl
10	65.4	4.3	2140	1	US-08-334-698-1	Sequence 1, Appli
11	65.4	4.3	2140	1	US-08-228-932-1	Sequence 1, Appli
12	65.4	4.3	2140	1	US-08-468-939-1	Sequence 1, Appli

Result No.	Score	Query Match	Length	DB	ID	Description
1	660.8	43.0	789	10	BI818538	BI818538 603033059
2	644.8	42.0	770	10	BI260681	BI260681 602968193
3	609.8	39.7	909	10	BE894106	BE894106 601438234
4	580.8	37.8	736	10	BI086726	BI086726 602850078
5	577.2	37.6	835	10	BF970560	BF970560 602274056
6	575	37.4	850	10	BI757207	BI757207 603030709
7	565.4	36.8	748	10	BG252201	BG252201 602365072
8	515.8	33.6	741	10	BG564220	BG564220 602586010
9	467.8	30.4	788	10	BF977798	BF977798 602148633
10	461.8	30.0	784	10	BI758685	BI758685 603024224

11	426.8	27.8	631	9	BB640431	BB640431 BB640431
12	426	27.7	819	10	BI088684	BI088684 602851458
13	423	27.5	424	10	BM194008	BM194008 TCAAP1E64
14	406.8	26.5	742	10	BI257225	BI257225 602976885
15	398.4	25.9	615	10	BF132059	BF132059 601821062

SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2117	100.0	402	21	AAB12827	Human 17723 recept
2	2117	100.0	402	21	AAY98008	Human G-protein co
3	2105	99.4	402	22	AAE12070	Dendritic cell (DC
4	1063	50.2	199	22	AAB64743	Human secreted pro
5	756	35.7	147	21	AAY32195	Human receptor mol
6	664	31.4	163	22	AAE12071	Dendritic cell (DC
7	664	31.4	879	22	AAU31008	Novel human secret
8	572	27.0	123	20	AAY60172	Human endometrium
9	564	26.6	122	21	AAB38327	Human secreted pro
10	459.5	21.7	349	10	AAP90554	Bovine rhodopsin.
11	455	21.5	348	17	AAR93116	Rhodopsin. Homo s
12	451	21.3	348	21	AAY98009	Human rhodopsin re
13	449	21.2	348	14	AAR38483	Rhodopsin protein.
14	424	20.0	354	21	AAY57086	Rhodopsin amino ac
15	420.5	19.9	309	15	AAR48735	G-protein coupled
16	420.5	19.9	309	17	AAW02707	G-protein coupled

RESULT 1
AAB12827
ID AAB12827 standard; Protein; 402 AA.
XX
AC AAB12827;
XX
DT 05-DEC-2000 (first entry)
XX
DE Human 17723 receptor protein SEQ ID NO:1.
XX
KW Human; 17723 receptor protein; chromosome 1q42-44; diagnosis; vaccine;
KW G-protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200043513-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-US01592.
XX
PR 21-JAN-1999; 99US-0234923.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA;
XX
DR WPI; 2000-476196/41.
DR N-PSDB; AAA73212.
XX
PT A G-protein-coupled receptor designated 17723 and the nucleic acids
PT that encode it, useful for preventing, diagnosing and treating disorder
PT associated with inappropriate expression of 17723 receptors -
XX
PS Claim 1; Page 70-72; 79pp; English.
XX
CC The present sequence is the human 17723 receptor protein (I), which

CC belongs to the superfamily of G-protein-coupled receptors. (I) and the
CC polynucleotide encoding it may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate 17723 receptor
CC expression. They may also be used to study the expression and function
CC of 17723 receptor polypeptides and their role in metabolism. The 17723
CC receptor polypeptides may be used as antigens in the production of
CC antibodies against 17723 receptors and in assays to identify modulators
CC (agonists and antagonists) of 17723 receptor expression and activity.
CC The anti-17723 receptor antibodies and 17723 receptor antagonists may be
CC used to down regulate 17723 receptor expression and activity. The
CC anti-17723 receptor antibodies may also be used as diagnostic agents for
CC detecting the presence of 17723 receptor polypeptides in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The 17723 receptor
CC protein has been mapped to chromosome 1q42-44.
XX
SQ Sequence 402 AA;

Query Match 100.0%; Score 2117; DB 21; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.3e-222;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mysgnrsgghgywdgggaagaegpapagtlspaplfspgtyerlalllgsigllgvgnnl 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 lvlvlyykfqrlrtpthlllvnislsdllvslfgvtftfvsclrngwvwdtvgcvwdgfs 120

Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwnryi 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ldvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcvedlqt 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 iqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylfaks 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ntvynpviyvfmirkfrrsllqllclrllrcqrpakdlpaagsemqirpivmsqkdgdrp 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
           |||||||||||||||||||||||||||||||||||||||||||
Db     361 kkkvtfnsssiifiitsdeslsvddsdktngskvdviqvrpl 402
```

RESULT 2
AAY98008
ID AAY98008 standard; Protein; 402 AA.
XX
AC AAY98008;
XX
DT 31-AUG-2000 (first entry)
XX
DE Human G-protein coupled receptor, HG51.
XX
KW Human; G-protein coupled receptor; HG51; signal transduction;
KW rhodopsin receptor; obesity; type II diabetes;
KW inflammatory bowel disease; constipation; diarrhoea; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200031108-A1.
XX
PD 02-JUN-2000.
XX

PF 18-NOV-1999; 99WO-US27305.
XX
PR 24-NOV-1998; 98US-0109717.
XX
PA (MERI) MERCK & CO INC.
XX
PI Liu Q, McDonald TP;
XX
DR WPI; 2000-400025/34.
DR N-PSDB; AAA38861.
XX
PT New DNA encoding human HG51 (a G-protein coupled receptor), useful in
PT chromosomal mapping studies for identifying the chromosomal locations
PT of the HG51 gene(s) -
XX
PS Claim 23; Fig 2; 68pp; English.
XX
CC G protein-coupled receptors (GPCR) are important in signal transduction
CC from the exterior to the interior of cells. Rhodopsin receptors are a
CC type of GPCR which comprise a chromophore-binding pocket which is
CC covalently linked by a protonated Schiff base to a Lys residue in
CC transmembrane domain 7. The present sequence is the human HG51 GPCR and
CC is a member of the rhodopsin receptor family of GPCRs. Due to the Lys
CC residue and Schiff base present in HG51, it is thought that the HG51
CC ligand may be a fatty-acid-like molecule. It is also believed that
CC agonists and antagonists of HG51 are useful for treating various
CC disorders such as obesity, type II diabetes, inflammatory bowel disease,
CC constipation or diarrhoea. In addition, the coding sequence for the
CC present sequence may be used in gene therapy for the above mentioned
CC disorders.
XX
SQ Sequence 402 AA;

Query Match 100.0%; Score 2117; DB 21; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.3e-222;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mysgnrsgghgywdgggaagaegpapagtlspaplfspgtyerlalllgsigllgvgnnl 60

Qy     61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 lvlvlyykfqrlrtpthlllvnislsdllvslfgvtftfvsclrngwvwdtvgcvwdgfs 120

Qy    121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwnryi 180

Qy    181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ldvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcvedlqt 240

Qy    241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 iqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylfaks 300

Qy    301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ntvynpviyvfmirkfrrsllqllclrllrcqrpakdlpaagsemqirpivmsqkdgdrp 360

Qy    361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
          |||||||||||||||||||||||||||||||||||||||||||
Db    361 kkkvtfnsssiifiitsdeslsvddsdktngskvdviqvrpl 402
```

RESULT 3
AAE12070
ID AAE12070 standard; Protein; 402 AA.
XX

AC AAE12070;
XX
DT 18-DEC-2001 (first entry)
XX
DE Dendritic cell (DC) DCEPR protein.
XX
KW Dendritic cell; DC; DCEPR protein; gene therapy; dermatological; vaccine;
KW atopic dermatitis; autoimmune disease; inflammatory skin disease; cancer;
KW immunosuppressive; AIDS; Acquired immune deficiency syndrome; cytostatic;
KW chromosomal identification; pharmaceutical; hypersensitivity; virucide;
KW transplant rejection; chronic inflammatory disease; anti-HIV.
XX
OS Unidentified.
XX
PN WO200172773-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-EP03542.
XX
PR 29-MAR-2000; 2000US-192934P.
PR 18-MAY-2000; 2000US-205020P.
PR 18-MAY-2000; 2000US-205026P.
PR 19-MAY-2000; 2000US-205767P.
PR 19-MAY-2000; 2000US-205769P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Werner G, Phares W, Jaritz M, Lapp H, Kalthoff FS;
XX
DR WPI; 2001-616466/71.
DR N-PSDB; AAD19720.
XX
PT New polypeptides for screening therapeutic agonists and antagonists
PT comprise dendritic cell polypeptides -
XX
PS Claim 2; Page 42; 52pp; English.
XX
CC The invention relates to dendritic cell (DC) proteins and their
CC corresponding DNA molecules. A pharmaceutical composition comprising
CC agonist and antagonist of DC proteins are useful for treating abnormal
CC conditions related to both an excess of and insufficient level of
CC expression of DC gene, or related to both an excess of and insufficient
CC activity of DC protein. Soluble form of DC proteins are used as an active
CC ingredient in combination with pharmaceutical acceptable carriers.
CC DC genes and proteins are useful for treating chronic inflammatory
CC diseases, autoimmune diseases, transplant rejection crisis, including
CC inflammatory skin diseases such as contact hypersensitivity, atopic
CC dermatitis or virally-induced immune suppression such as AIDS and cancer.
CC DC protein is useful for inducing immunological response in a mammal, and
CC as immunogen to produce antibodies immunospecific for the polypeptide.
CC DC gene is useful in gene therapy. DC gene is also useful as a diagnostic
CC reagent, and for chromosomal identification. The present sequence is
CC dendritic cell (DC) DCEPR protein which is found to belong to the family
CC of G-protein coupled receptor protein.
XX
SQ Sequence 402 AA;

Query Match 99.4%; Score 2105; DB 22; Length 402;
Best Local Similarity 99.5%; Pred. No. 1.3e-220;
Matches 400; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
           |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       1 mysgnrsgghgywdgggaagakgpapagtlspaplfspgtyerlalllgsigllgvgnnl 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 lvlvlyykfqrlrtpthlllvnislsdllvslfgvtftfvsclrngwvwdtvgcvwdgfs 120
```

```
Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwnryi 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ldvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcvedlqt 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 iqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylfaks 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ntvynpviyvfmirkfrrsllqllclrllrcqrpakdlpaagsemqirpivmsqkdgdrp 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
           ||||||||||||| ||||||||||||||||||||||||||||
Db     361 kkkvtfnsssiifigtsdeslsvddsdktngskvdviqvrpl 402
```

RESULT 4
AAB64743
ID AAB64743 standard; Protein; 199 AA.
XX
AC AAB64743;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:137.
XX
KW Human; secreted protein; diagnosis; cytostatic; antirheumatic;
KW antiarthritic; dermalogical; cardiant; antiinflammatory; anti-ulcer;
KW gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; myocardial angiogenesis; Crohn's disease;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200077237-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US14928.
XX
PR 11-JUN-1999; 99US-0138633.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-071280/08.
XX
PT Nucleic acids encoding 49 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating diseases such as tumors,
PT rheumatoid arthritis, psoriasis and diabetic retinopathy -
XX
PS Disclosure; Page 503; 520pp; English.
XX
CC The polynucleotide sequences given in AAF33037 to AAF33085 encode the
CC human secreted proteins given in AAB64666 to AAB64714. AAB64715 to
CC AAB64771 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC cytostatic; antirheumatic; antiarthritic; dermalogical; cardiant;
CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides
CC and polypeptides can be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate polypeptide expression.

CC Disorders that may be treated or prevented include solid tumours,
CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial
CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate
CC the presence of similar nucleic acid sequences in samples, and therefore
CC which patients may be in need of restorative therapy. The polypeptides
CC may also be used as antigens in the production of antibodies against the
CC polypeptide and in assays to identify modulators (agonists and
CC antagonists) of polypeptide expression and activity. The anti-polypeptide
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 199 AA;

Query Match 50.2%; Score 1063; DB 22; Length 199;
Best Local Similarity 100.0%; Pred. No. 2e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    118 GFSGSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWN 177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gfsgslfgivsiatltvlayeryirvvharvinfswawraityiwlyslawagapllgwn 60

Qy    178 RYILDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVED 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ryildvhglgctvdwkskdandssfvlflflgclvvplgviahcyghilysirmlrcved 120

Qy    238 LQTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLF 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 lqtiqvikilkyekklakmcflmiftflvcwmpyivicflvvnghghlvtptisivsylf 180

Qy    298 AKSNTVYNPVIYVFMIRKF 316
          ||||||||||||||||||
Db    181 aksntvynpviyvfmirkf 199
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	451	21.3	348	2	US-08-390-000A-8	Sequence 8, Appli
2	444	21.0	348	4	US-08-430-286A-11	Sequence 11, Appl
3	420.5	19.9	309	1	US-08-118-270-56	Sequence 56, Appl
4	420.5	19.9	309	5	PCT-US93-08528-56	Sequence 56, Appl
5	354.5	16.7	297	1	US-08-118-270-58	Sequence 58, Appl
6	354.5	16.7	297	5	PCT-US93-08528-58	Sequence 58, Appl
7	341.5	16.1	305	1	US-08-118-270-59	Sequence 59, Appl
8	341.5	16.1	305	5	PCT-US93-08528-59	Sequence 59, Appl
9	338.5	16.0	297	1	US-08-118-270-57	Sequence 57, Appl
10	338.5	16.0	297	5	PCT-US93-08528-57	Sequence 57, Appl
11	309	14.6	391	1	US-07-816-283-2	Sequence 2, Appli
12	309	14.6	391	1	US-08-417-103-2	Sequence 2, Appli
13	309	14.6	391	1	US-08-417-103-14	Sequence 14, Appl
14	304	14.4	391	1	US-07-816-283-4	Sequence 4, Appli
15	304	14.4	391	1	US-08-417-103-4	Sequence 4, Appli

Result No.	Score	Query Match	Length	DB	ID	Description
1	477.5	22.6	349	1	JC5490	opsin, pineal glan
2	475	22.4	351	1	A55962	opsin, pineal glan
3	464	21.9	352	2	I50081	rhodopsin - green
4	458	21.6	348	1	OOBO	rhodopsin - bovine
5	456.5	21.6	348	1	JC4267	opsin - rabbit
6	455	21.5	348	1	S23398	rhodopsin - Chines
7	452.5	21.4	351	2	S29152	rhodopsin - chicke

8	451	21.3	348	1	OOHU	rhodopsin - human
9	451	21.3	354	1	S27231	rhodopsin - northe
10	450	21.3	348	1	A23665	opsin - mouse
11	448	21.2	354	1	I51200	rhodopsin - Africa

Result No.	Score	Query Match	Length	DB	ID	Description
1	2117	100.0	402	1	OPN3_HUMAN	Q9h1y3 homo sapien
2	1862	88.0	400	1	OPN3_MOUSE	Q9wuk7 mus musculu
3	477.5	22.6	349	1	OPSP_COLLI	P51476 columba liv
4	475	22.4	351	1	OPSP_CHICK	P51475 gallus gall
5	468	22.1	352	1	OPSD_ALLMI	P52202 alligator m
6	466.5	22.0	444	1	OPSP_PETMA	O42490 petromyzon
7	464	21.9	352	1	OPSD_ANOCA	P41591 anolis caro
8	458	21.6	348	1	OPSD_BOVIN	P02699 bos taurus
9	456.5	21.6	348	1	OPSD_RABIT	P49912 oryctolagus
10	455	21.5	348	1	OPSD_CRIGR	P28681 cricetulus
11	455	21.5	348	1	OPSD_MACFA	Q28886 macaca fasc
12	455	21.5	354	1	OPSD_RANCA	P51470 rana catesb

```
RESULT   1
OPN3_HUMAN
ID   OPN3_HUMAN     STANDARD;      PRT;   402 AA.
AC   Q9H1Y3; Q9Y344;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Opsin 3 (Encephalopsin) (Panopsin).
GN   OPN3 OR ECPN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99252448; PubMed=10234000;
RA   Blackshaw S., Snyder S.H.;
RT   "Encephalopsin: a novel mammalian extraretinal opsin discretely
RT   localized in the brain.";
RL   J. Neurosci. 19:3681-3690(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21295039; PubMed=11401433;
RA   Halford S., Freedman M.S., Bellingham J., Inglis S.L.,
RA   Poopalasundaram S., Soni B.G., Foster R.G., Hunt D.M.;
RT   "Characterization of a novel human opsin gene with wide tissue
RT   expression and identification of embedded and flanking genes on
RT   chromosome 1q43.";
RL   Genomics 72:203-208(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Parker A.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May play a role in encephalic photoreception.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Strongly expressed in brain. Highly expressed
CC       in the preoptic area and paraventricular nucleus of the
CC       hypothalamus. Shows highly patterned expression in other regions
CC       of the brain, being enriched in selected regions of the cerebral
CC       cortex, cerebellar Purkinje cells, a subset of striatal neurons,
CC       selected thalamic nuclei, and a subset of interneurons in the
CC       ventral horn of the spinal cord.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       OPSIN SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
```

```
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF140242; AAD32671.1; -.
DR   EMBL; AF303588; AAK37447.1; -.
DR   EMBL; AL133390; CAC19785.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00238; OPSIN; 1.
KW   Photoreceptor; Retinal protein; Transmembrane; Lipoprotein; Palmitate;
KW   G-protein coupled receptor.
FT   DOMAIN        1     40       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     41     65       1 (POTENTIAL).
FT   DOMAIN       66     77       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78    102       2 (POTENTIAL).
FT   DOMAIN      103    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    118    137       3 (POTENTIAL).
FT   DOMAIN      138    153       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    154    177       4 (POTENTIAL).
FT   DOMAIN      178    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    229       5 (POTENTIAL).
FT   DOMAIN      230    255       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    256    279       6 (POTENTIAL).
FT   DOMAIN      280    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    312       7 (POTENTIAL).
FT   DOMAIN      313    402       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    114    188       BY SIMILARITY.
FT   BINDING     299    299       RETINAL CHROMOPHORE.
FT   LIPID       325    325       PALMITATE (BY SIMILARITY).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    390    396       NGSKVDV -> IGVQSLML (IN REF. 1).
SQ   SEQUENCE   402 AA;  44873 MW;  370F64C19F834A71 CRC64;


  Query Match             100.0%;  Score 2117;  DB 1;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 1e-136;
  Matches  402;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL 60

Qy      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS 120

Qy     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI 180

Qy     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT 240

Qy     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS 300

Qy     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP 360

Qy     361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402
           |||||||||||||||||||||||||||||||||||||||||||
```

Db 361 KKKVTFNSSSIIFIITSDESLSVDDSDKTNGSKVDVIQVRPL 402

Result No.	Score	% Query Match	Length	DB	ID	Description
1	500.5	23.6	352	13	Q9W6K3	Q9w6k3 anolis caro
2	491.5	23.2	534	13	O57422	O57422 xenopus lae
3	484.5	22.9	346	13	Q9PUA9	Q9pua9 bufo japoni
4	480	22.7	357	13	Q9IBH2	Q9ibh2 phelsuma ma
5	473.5	22.4	377	13	Q9IB88	Q9ib88 brachydanio
6	473	22.3	543	13	Q90YK6	Q90yk6 gallus gall
7	458	21.6	348	6	Q95KU1	Q95ku1 felis silve
8	457.5	21.6	351	13	Q9IA36	Q9ia36 poephila gu
9	455.5	21.5	351	13	Q9W6S0	Q9w6s0 columba liv
10	455	21.5	363	13	Q98TH3	Q98th3 cynops pyrr
11	453.5	21.4	322	13	O57448	O57448 anas platyr